

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 22, 2002, 15:37:06 ; Search time 13.4 Seconds
(Without alignments) 944.873 Million cell updates/sec

Title: US-09-771-209-76

Perfect score: 1687
Sequence: 1 MERRHSGVSEFVLGPPA.....RTLHLAQDEANTNGSKTG 327

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	1680	99.6	327	1	OLF7_RAT
2	1432	84.9	327	1	OLF7_RAT
3	957.5	56.8	311	1	OLF6_HUMAN
4	788	46.7	311	1	OLF6_RAT
5	751	44.5	222	1	OLF6_MOUSE
6	719.5	42.6	317	1	OLFA5_HUMAN
7	711.5	42.2	321	1	OLFA5_HUMAN
8	710.5	42.1	315	1	OLFA4_HUMAN
9	709	42.0	312	1	OLFA1_HUMAN
10	697.5	41.3	315	1	OLFA1_HUMAN
11	688.5	40.8	314	1	OLFA1_HUMAN
12	671	39.8	316	1	OLFA3_HUMAN
13	670	39.7	357	1	OLFA2_HUMAN
14	669	39.7	312	1	OLFA2_HUMAN
15	667	39.5	313	1	OLFA2_HUMAN
16	665	39.4	313	1	OLFA2_HUMAN
17	663	39.3	311	1	OLFA1_HUMAN
18	662.5	39.3	313	1	OLFA1_HUMAN
19	659.5	39.1	314	1	OLFA1_HUMAN
20	656	38.9	319	1	OLFA2_HUMAN
21	653.5	38.7	320	1	OLFA2_HUMAN
22	650.5	38.6	311	1	OLFA2_HUMAN
23	650.5	38.6	313	1	OLFA2_HUMAN
24	649	38.5	308	1	OLFA2_HUMAN
25	644	38.2	312	1	OLFA2_HUMAN
26	644	38.2	318	1	OLFA2_HUMAN
27	642.5	38.1	314	1	OLFA2_HUMAN
28	640	37.9	315	1	OLFA2_HUMAN
29	638	37.8	316	1	OLFA2_HUMAN
30	636.5	37.7	313	1	OLFA2_HUMAN
31	636	37.7	320	1	OLFA2_HUMAN
32	635	37.6	314	1	OLFA2_HUMAN
33	634.5	37.6	312	1	OLFA2_HUMAN

34	632.5	37.5	312	1	OLFA1_HUMAN	043749 homo sapien
35	631	37.4	315	1	OLFA2_HUMAN	060403 homo sapien
36	629	37.3	317	1	OLFA2_HUMAN	013607 homo sapien
37	628.5	37.3	320	1	OLFA2_HUMAN	060412 homo sapien
38	627.5	37.2	311	1	OLFA2_HUMAN	076001 homo sapien
39	627	37.2	317	1	OLFA2_HUMAN	095156 canis fam1
40	626.5	37.1	313	1	OLFA2_HUMAN	047890 homo sapien
41	625	37.0	312	1	OLFA2_HUMAN	095371 homo sapien
42	624	37.0	309	1	OLFA2_HUMAN	095371 homo sapien
43	623	36.9	312	1	OLFA2_HUMAN	095371 homo sapien
44	623	36.9	314	1	OLFA2_HUMAN	095371 homo sapien
45	621.5	36.8	307	1	OLFA2_HUMAN	058182 homo sapien

ALIGNMENTS

RESULT	ID	STANDARD	PRT	AA
1	OLF7_RAT			
AC	P23270			
DT	01-NOV-1991 (Rel. 20, Created)			
DT	01-NOV-1991 (Rel. 20, Last sequence update)			
DT	01-JUL-1993 (Rel. 26, Last annotation update)			
DE	Olfactory receptor-like protein 17.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91191556; PubMed=1840504;			
RA	Buck L., Axel R.;			
RT	"A novel multigene family may encode odorant receptors: a molecular			
RT	basis for odor recognition."			
RL	Cell 65:175-187(1991).			
CC	-1- FUNCTION: PUTATIVE ODORANT RECEPTOR.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL; M64386; AAA41749.1; -			
DR	PIR; F23701; F23701.			
DR	GCRDB; GCR_0148; -			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00245; OLFACTORYR.			
DR	PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.			
DR	PROSITE; PS50262; G-PROTEIN_RECEP_FL_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	Multigene family; Olfaction.			
FT	DOMAIN	1	26	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	27	50	1 (POTENTIAL).
FT	DOMAIN	51	58	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	59	80	2 (POTENTIAL).
FT	DOMAIN	81	104	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	105	125	3 (POTENTIAL).
FT	DOMAIN	126	144	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	145	163	4 (POTENTIAL).
FT	DOMAIN	164	201	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	202	224	5 (POTENTIAL).
FT	DOMAIN	225	241	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	242	265	6 (POTENTIAL).
FT	DOMAIN	266	277	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	278	297	7 (POTENTIAL).

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FT DOMAIN 298 327 CYTOPLASMIC (POTENTIAL).
FT CAROHD 5 5 N-LINKED (GLCNMC. . .) (POTENTIAL).
FT DISULFID 102 194 BY SIMILARITY.
SQ SEQUENCE 327 AA: 36265 MW: 85863DE961621D9 CRC64:

Query Match
Best Local Similarity 99.6%; Score 1680; DB 1; Length 327;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MERRNSGRVSEFVLLGFPAPAPARVLLFELSLDYLVLTENMLIIAIRNHPHLHKPM 60
DB 1 MERRNSGRVSEFVLLGFPAPAPARVLLFELSLDYLVLTENMLIIAIRNHPHLHKPM 60
OY 61 YFFLANMSFLEIYVTVTPKMLAGFTSGKENHGOLISEPACTOLYFFLGICTECVLL 120
DB 61 YFFLANMSFLEIYVTVTPKMLAGFTSGKENHGOLISEPACTOLYFFLGICTECVLL 120
OY 121 AYMAVDYVAICHPPLHYPIYVSRLCVQMAAGSMAGGFGISMKVPLISRLSYCGPNTIN 180
DB 121 AYMAVDYVAICHPPLHYPIYVSRLCVQMAAGSMAGGFGISMKVPLISRLSYCGPNTIN 180
OY 181 HFECDVSPLLNSTCDTMSAEITDFVLAIFILLGPLSVTGASYMATGAVMRIPSAAGR 240
DB 181 HFECDVSPLLNSTCDTMSAEITDFVLAIFILLGPLSVTGASYMATGAVMRIPSAAGR 240
OY 241 KAFSTCASHLVTVITFYASIFLYARPKALSAFDTKLVSVLYAVVPLFNPIIYCLRNQ 300
DB 241 KAFSTCASHLVTVITFYASIFLYARPKALSAFDTKLVSVLYAVVPLFNPIIYCLRNQ 300
OY 301 DVKRALRTLHLAODQEAANTNKGSKIG 327
DB 301 DVKRALRTLHLAODQEAANTNKGSKIG 327

RESULT 2
O6A1_HUMAN STANDARD: PRT: 327 AA.
ID 06A1_HUMAN
AC 095222:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Olfactory receptor 6A1 (Olfactory receptor 11-55) (OR11-55).
GN OR6A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99005533; PubMed=9787077;
RA Buettner J.A., Glusman G., Ben-Arie N., Ramos P., Lancel D.,
RA Evans G.A.;
RT "Organization and evolution of olfactory receptor genes on human
RT chromosome 11."
RL Genomics 53:56-68(1998).
CC -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AF065870; AAC70018.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHDODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; FALSE_NEG.
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DR PROSITE: PS00262; G_PROTEIN_RECIP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KM Multigene family; Olfaction.
FT DOMAIN 1 26
FT TRANSMEM 27 50
FT DOMAIN 51 58
FT TRANSMEM 59 80
FT DOMAIN 81 105
FT TRANSMEM 106 125
FT DOMAIN 126 144
FT TRANSMEM 145 163
FT TRANSMEM 164 201
FT TRANSMEM 202 224
FT DOMAIN 225 241
FT TRANSMEM 242 264
FT DOMAIN 265 277
FT TRANSMEM 278 297
FT DOMAIN 298 320
FT DISULFID 102 194
FT CAROHD 5 5
FT CAROHD 191 191
SQ SEQUENCE 327 AA: 36049 MW: 69956A573ECFDA04 CRC64:

Query Match
Best Local Similarity 84.9%; Score 1432; DB 1; Length 327;
Matches 281; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

OY 1 MERRNSGRVSEFVLLGFPAPAPARVLLFELSLDYLVLTENMLIIAIRNHPHLHKPM 60
DB 1 MERRNSGRVSEFVLLGFPAPAPARVLLFELSLDYLVLTENMLIIAIRNHPHLHKPM 60
OY 61 YFFLANMSFLEIYVTVTPKMLAGFTSGKENHGOLISEPACTOLYFFLGICTECVLL 120
DB 61 YFFLANMSFLEIYVTVTPKMLAGFTSGKENHGOLISEPACTOLYFFLGICTECVLL 120
OY 121 AYMAVDYVAICHPPLHYPIYVSRLCVQMAAGSMAGGFGISMKVPLISRLSYCGPNTIN 180
DB 121 AYMAVDYVAICHPPLHYPIYVSRLCVQMAAGSMAGGFGISMKVPLISRLSYCGPNTIN 180
OY 181 HFECDVSPLLNSTCDTMSAEITDFVLAIFILLGPLSVTGASYMATGAVMRIPSAAGR 240
DB 181 HFECDVSPLLNSTCDTMSAEITDFVLAIFILLGPLSVTGASYMATGAVMRIPSAAGR 240
OY 241 KAFSTCASHLVTVITFYASIFLYARPKALSAFDTKLVSVLYAVVPLFNPIIYCLRNQ 300
DB 241 KAFSTCASHLVTVITFYASIFLYARPKALSAFDTKLVSVLYAVVPLFNPIIYCLRNQ 300
OY 301 DVKRALRTLHLAODQEAANTNKGSK 325
DB 301 DVKRALRTLHLAODQEAANTNKGSK 325
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RESULT 3
O6B1_HUMAN STANDARD: PRT: 311 AA.
ID 06B1_HUMAN
AC 095007:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Olfactory receptor 6B1 (Olfactory receptor 7-3) (OR7-3).
GN OR6B1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bauer C., Williams D.;
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL: AC004853; AAC64377.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECPR_FL_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECPR_FL_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
KM Multigene family; Olfaction.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 26 49 1 (POTENTIAL).
FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 58 79 2 (POTENTIAL).
FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 120 3 (POTENTIAL).
FT DOMAIN 121 139 4 (POTENTIAL).
FT TRANSMEM 140 158 4 (POTENTIAL).
FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 196 219 5 (POTENTIAL).
FT DOMAIN 220 234 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 235 257 6 (POTENTIAL).
FT DOMAIN 258 270 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 271 290 7 (POTENTIAL).
FT DOMAIN 291 311 CYTOPLASMIC (POTENTIAL).
FT DISULFID 97 189 BY SIMILARITY.
FT CARBOHYD 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 311 AA: 35299 MW: 671FD19658FE0616 CRC64;

Query Match 56.8%; Score 957.5; DB 1; Length 311;
Best Local Similarity 56.8%; Pred. No. 5e-67;
Matches 175; Conservative 54; Mismatches 72; Indels 7; Gaps 3;

OY 1 MERRNHGSEFVLLGPAPAPLRLVLLFSLDYLVLVTENMLIIAIRNHPPLHKKM 60
DB 1 MELENOT-RVTKFLLVFGSLMRAMPFLPLVAVILVAVENVAIIILLVQNRPLHKM 59
OY 61 YFFLANSLFETWYISVYVPKLLFSEFVSNNNS---ISFTLCMIQLYFFIALMCTEYDL 120
DB 60 YFFLANSLFETWYISVYVPKLLFSEFVSNNNS---ISFTLCMIQLYFFIALMCTEYDL 115
OY 121 AVMAVDYVAICHPPLVPIVYSRLCYOMAGSMAGSGFISWVKFLLISLSCGPNTIN 180
DB 116 AAMAVDRYVAICRPLHPIYRIMSHGLCFRLALGSMALIGRISLAKIYFISLSCFQPNVIN 175
OY 181 HFFCDVSPLLNSCTDMSTAEFLDFVLAIFLLGLPSVTGASYMAITGAVMRIPSAAGR 240
DB 176 HFFCDISPVLNLSCTDMSTAEFLDFVLAIFLLGLPSVTGASYMAITGAVMRIPSAAGR 240
OY 241 KAFSCASHLVVYVIFVYASIFIVARPKRLSAFDNKLVSIVXAVIVLFFNIIYICLRQ 300
DB 234 KAFSCASHLVVYVIFVYASIFIVARPKRLSAFDNKLVSIVXAVIVLFFNIIYICLRQ 300
OY 301 DVKRALRR 308
DB 294 EVKALKK 301

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DE Olfactory receptor-like protein F6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91191556; PubMed=1840504;
RA Buck L., Axel R.;
RT "A novel multigene family may encode odorant receptors: a molecular
RT basis for odor recognition.";
RL Cell 65:175-187(1991).
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: M64378; AAA41741.1; -
DR PIR: C23701; C23701.
DR GCRDB: GCR_0146; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00245; OLFACTORYR.
DR PROSITE: PS00237; G-PROTEIN_RECPR_FL_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECPR_FL_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
KM Multigene family; Olfaction.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 53 1 (POTENTIAL).
FT DOMAIN 54 60 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 61 82 2 (POTENTIAL).
FT DOMAIN 83 103 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 104 123 3 (POTENTIAL).
FT DOMAIN 124 142 4 (POTENTIAL).
FT TRANSMEM 143 161 4 (POTENTIAL).
FT DOMAIN 162 199 5 (POTENTIAL).
FT TRANSMEM 200 222 5 (POTENTIAL).
FT DOMAIN 223 239 6 (POTENTIAL).
FT TRANSMEM 240 263 6 (POTENTIAL).
FT DOMAIN 264 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 295 7 (POTENTIAL).
FT DOMAIN 296 311 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 100 192 BY SIMILARITY.
SQ SEQUENCE 311 AA: 34168 MW: 9E092CFE85A58BF1 CRC64;

Query Match 46.7%; Score 788; DB 1; Length 311;
Best Local Similarity 50.7%; Pred. No. 5.8e-54;
Matches 151; Conservative 46; Mismatches 97; Indels 4; Gaps 1;

OY 13 FVLGFPAPAPLRLVLLFSLDYLVLVTENMLIIAIRNHPPLHKKMVFLLANNSFLEI 72
DB 15 FILLGFPAPAPLRLVLLFSLDYLVLVTENMLIIAIRNHPPLHKKMVFLLANNSFLEI 74
OY 73 WYVYVIRKMLAGFTGSKENHQLISFECMQLYFFLGLGTEBEVLLAVMAVDYVAIC 132
DB 75 WFTACVPRPLATF---APRGVITSLAGCAQOMVFESLGTETVLLAVMAVDYVAIC 130
OY 133 HPLHPIVSSRLCYOMAGSMAGSGFISWVKFLLISLSCGPNTINHPFCDVSPLLN 192
DB 131 LPLRIGGIMTPELAKRLALGSLGFSATYVATILARSLGSGKRVINHPFCDISPVL 190
OY 193 SCTDMSTAEFLDFVLAIFLLGLPSVTGASYMAITGAVMRIPSAAGRKAFTSCASHLV 252
DB 111 SCTDMSTAEFLDFVLAIFLLGLPSVTGASYMAITGAVMRIPSAAGRKAFTSCASHLV 252

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[illegible]

ID	NAME	SEQUENCE	FUNCTION	REFERENCE
Db	1	YELSTMSELEANYISVTPYKMLAGFL---	HPNPNTISFLGCGTQLYLPFMSLACTFCVLLA	56
Qy	122	WAATRYVAICHPRLPPIVYSRLCYQMAAGSAGGEGISMKVYLLISRLSCGNTINH	181	
Db	57	AAAYRYVAICHPRLPPIVYSRLCYQMAAGSAGGEGISMKVYLLISRLSCGNTINH	116	
Qy	182	FFCDVSPPLINLSCTMTSAELTDFVLAIFILLGLPSVSGASYMAITGAVMRIPSAAGRHK	241	
Db	117	FFCDVSPPLINLSCTMTSAELTDFVLAIFILLGLPSVSGASYMAITGAVMRIPSAAGRHK	176	
Qy	242	AFSTCASHLTVVITFYAASIFFYARPKALSAFDTKKLVSLYAV	285	
Db	177	AFSTCASHLTVVITFYAASIFFYARPKALSAFDTKKLVSLYAV	220	
RESULT	6			
OAA5_HUMAN				
AC	Q9H207	STANDARD	PRT	317 AA.
DT	16-OCT-2001	(Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	01-MAR-2002	(Rel. 41, Last annotation update)		
DE	Olfactory receptor 10A5 (HB3) (Putative taste receptor JCG6).			
GN	OR10A5.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Lane R.P., Culicforth T., Young J., Athanasios M., Friedman C.,			
RA	Rosen L., Evans G., Axel R., Hood L., Trask B.J.;			
RT	"Genomic analysis of orthologous mouse and human olfactory receptor			
RT	loci indicates cluster stability yet minimal conservation beyond the			
RT	coding sequence.";			
RL	Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Tongue;			
RX	MEDLINE=21562400; Pubmed=11705801;			
RA	Gaudin J.C., Breuils L., Haerle T.;			
RA	"New GPCRs from a human lingual cDNA library.";			
RL	Chem. Senses 26:1157-1166(2001).			
CC	-1- FUNCTION: PUTATIVE ODORANT RECEPTOR.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	-----			
DR	EMBL: AF321237; AAG45206.1; -			
DR	EMBL: AF324499; AA133005.1; -			
DR	InterPro: IPR000276; GPCR_Rhoipn.			
DR	Pfam: PF00001; 7tm_L1; 1.			
DR	PRINTS: PR00237; GPCR_RHOPOPSN.			
DR	PROSITE: PS00237; G-PROTEIN_RECEP_FL1; 1.			
DR	PROSITE: PS50262; G-PROTEIN_RECEP_FL2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	Multigene family; Olfaction.			
FT	DOMAIN	1	26	
FT	TRANSMEM	27	30	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	51	58	1 (POTENTIAL).
FT	TRANSMEM	59	80	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	81	101	2 (POTENTIAL).
FT	TRANSMEM	102	121	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	122	140	3 (POTENTIAL).
FT	TRANSMEM	141	159	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	160	196	4 (POTENTIAL).
FT	DOMAIN			EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 197 220 5 (POTENTIAL).
 FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 238 260 6 (POTENTIAL).
 FT DOMAIN 261 273 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 274 293 7 (POTENTIAL).
 FT DOMAIN 294 317 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 98 190 BY SIMILARITY.
 FT CARBOHYD 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 317 AA; 35519 MW; 464073EFC4ECSB45 CRC64;

Query Match 42.6%; Score 719.5; DB 1; Length 317;
 Best Local Similarity 46.9%; Pred. No. 1.1e-48;
 Matches 142; Conservative 48; Mismatches 108; Indels 5; Gaps 2;

QY 10 USEFVLGEPAPAPRLVLFELSLDYVLTENMLIIAIRNHPTLHKPFYFLANKS 68
 DB 9 ISEFLMSESSLPTEIOSLFLFTFLTYLVTLKGNLSLIIVTLADPMLHSPMYFELRNLS 68
 QY 69 FLEIYVVTVPKMLAGFSGKENHGOISFEACMTOLYFELGLCTECVLLAVAYDREY 128
 DB 69 FLEIFGNLYVYKMKLTLLAODT-----ISFLGCATOMYFFFFRGAECFLLATMAYDRY 124
 QY 129 VAICPHLYPVIVSSRLCVQMAAGSGAGFGISMWKVELISRLSYCGPNTINHFECVSP 188
 DB 125 VAICSPHLYPVIMQRTAKLAAASMPGPGVATVQTWTLFSGPGCTNKVNHFFCDSP 184
 QY 189 LLNLSTDMSTAEITDPLVLAIFILGLPLSVTGSYMAITGAVMRIPSAAGRAKASTCAS 248
 DB 185 VKLVLCAPTALFEIYAIYGTILVWIMPCLLICSVYTRIAALIKIPSAAGRAKASTCAS 244
 QY 249 HLTVAIIFEASIFIYAPRKALSAFDTKKIVSLVAVIYVPLEPNTIYCLRNODVRAALRR 308
 DB 245 HLTVAIIFEASIFIYAPRKALSAFDTKKIVSLVAVIYVPLEPNTIYCLRNODVRAALRR 304
 QY 309 TLH 311
 DB 305 TFH 307

RESULT 7
 05VL_HUMAN STANDARD; PRT; 321 AA.
 AC 09GGE6:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Olfactory receptor 5V1 (Hs6M1-21).
 GN OR5V1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN NCI
 RP SEQUENCE FROM N.A.
 RA Tracey A.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 or send an email to license@isb-sib.ch).
 CC EMBL; AL096770; CAB65797.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECPEP_F1_1;
 DR PROSITE; PS00262; G_PROTEIN_RECPEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT TRANSMEM 26 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 79 2 (POTENTIAL).
 FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 101 120 3 (POTENTIAL).
 FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 140 158 4 (POTENTIAL).
 FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 196 219 5 (POTENTIAL).
 FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 237 259 6 (POTENTIAL).
 FT DOMAIN 260 272 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 273 292 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 293 321 BY SIMILARITY.
 FT DISULFID 97 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 5
 SQ SEQUENCE 321 AA; 36056 MW; AAC426FDC58E375 CRC64;

Query Match 42.2%; Score 711.5; DB 1; Length 321;
 Best Local Similarity 45.9%; Pred. No. 4.7e-48;
 Matches 141; Conservative 56; Mismatches 105; Indels 5; Gaps 2;

QY 1 MERRNHSGRVSEFVLGPPAPRLVLFELSLDYVLTENMLIIAIRNHPTLHKPK 60
 DB 1 MERKQTA-ITFEIILGFSNLNELQFLFTIFELTYECLGNIILITVTDPHLP 59
 QY 61 YEFLLMSLEIYVVTIPKMLAGFSGKENHGOISFEACMTOLYFELGLCTECVLL 120
 DB 60 YFELGLAEITDICTYTSNPOHMHLSKRKS----ISYGCVOQLFAVVFYGSCLLL 115
 QY 121 AVMAVDYVAICPHLYPVIVSSRLCVQMAAGSGAGFGISMWKVELISRLSYCGPNTIN 180
 DB 116 AVMAVDYVAICPHLYPVIVSSRLCVQMAAGSGAGFGISMWKVELISRLSYCGPNTIN 175
 QY 181 HFECDVSPLLNLSCDTMSTAEITDPLVLAIFILGLPLSVTGSYMAITGAVMRIPSAAGR 240
 DB 176 YFECDDPPLLILSCGWTGVTNELALISTGVETGTPCLIVSLICITSLIRIQSEGR 225
 QY 241 KAFSTCASHLIYVVIIFYAASIFLYAPRKALSAFDTKKIVSLVAVIYVPLEPNTIYCLRNQ 300
 DB 236 KAFSTCASHLIYVVIIFYAASIFLYAPRKALSAFDTKKIVSLVAVIYVPLEPNTIYCLRNQ 295
 QY 301 DVKRALR 307
 DB 296 DIKEAVK 302

RESULT 8
 0AA4_HUMAN STANDARD; PRT; 315 AA.
 AC 09H209:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Olfactory receptor 10A4 (HP2).
 GN OR10A4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN NCI
 RP SEQUENCE FROM N.A.
 RA Lane R.P., Cutforth T., Young J., Athanasou M., Friedman C.,
 RA Rowen U., Evans G., Axel R., Hood L., Trask B.J.;
 RT "Genomic analysis of orthologous mouse and human olfactory receptor
 RT loci indicates cluster stability yet minimal conservation beyond the
 RT coding sequence.";

CC	EMBL; AF065863; AAC70017.1; -	
DR	InterPro; IPR000276; GPCR_Rhodopsn.	
DR	Pfam; PF00001; 7tm_1; 1.	
DR	PRINTS; P000237; GPCR_RHODOPSIN.	
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.	
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.	
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;	
KW	Multiene family; Olfaction.	
FT	DOMAIN	1 25
FT	TRANSMEM	26 49
FT	DOMAIN	50 57
FT	TRANSMEM	58 79
FT	DOMAIN	80 100
FT	TRANSMEM	101 120
FT	DOMAIN	121 139
FT	TRANSMEM	140 158
FT	DOMAIN	159 195
FT	TRANSMEM	196 219
FT	DOMAIN	220 236
FT	TRANSMEM	237 252
FT	DOMAIN	260 279
FT	TRANSMEM	273 292
FT	DOMAIN	293 314
FT	DISULFID	97 189
FT	CARBOHYD	5 5
QO	SEQUENCE	314 AA; 35131 MW; C14A9A25CD6BEA3 CRC64; N-LINKED (GLCNAC. .) (POTENTIAL)

FT CONFLICT 307 311 RDSRE -> MGITQ (IN REF. 2).
SQ SEQUENCE 316 AA; 35410 MW; BE29B672B663A7CE CRC64;

Query Match
Best Local Similarity 46.2%; Pred. No. 6.1e-45;
Matches 140; Conservative 46; Mismatches 113; Indels 4; Gaps 1;

QY 13 FVLGGFAPAPARLVLFLLSLDDVVLVTEMLIIAIRNHPFLHKAHPYFLANMSFLEI 72
10 FLLGFSSEHPLEKTLVVVFTSLTLVGTLLILSALDPKLIHSPYFLSLMSFLDL 69
DB 10 FLLGFSSEHPLEKTLVVVFTSLTLVGTLLILSALDPKLIHSPYFLSLMSFLDL 69
QY 73 WYVVTIPKMLAGFISGENHGLISFEACMTQLYFGLGCTECVLLAVAYRYAIC 132
DB 70 CFTTSCVPMVLVNMGRKT----ISFLDCSVQIFIFLSLGTTCIILTYMAFPYRYAVC 125
QY 133 HPLHYPIVYSSRLCYVMAAGSMAGGFGISMKVYFLISRLSYCGPNTINHFECVSPILN 192
DB 126 QPLHYATIIHPRLCOMQLASVAVMIGLVESVYQTPSTLHLFECPPDQVDFCEVPALIRL 185
QY 193 SCTDMSTAEITDFVLAIFILLGLPSVTGASYMATGAVMRIPSAAGHKAFTCSHLTV 252
DB 186 SCBPTSTNEIOVAVASFIPLVPLSLVIGAITMAVLRINSAKGRKAFGTCSSHLTV 245
QY 253 VTIIFYASIFITYARPKALSAFDTNKLVSIVYAVIPFNPIYICLRNODVYKALRRLHL 312
DB 246 VTLFYSVIVAYIOPKPNYQAEGRKFGFLFAYVGTSPSLNPLITYLRNKEVYRARRLLGK 305
QY 313 AOD 315
DB 306 ERD 308

RESULT 13
O2B2_HUMAN STANDARD; PRT; 357 AA.
ID O2B2_HUMAN
AC O9GZK3; O9GZL2; O9Y299;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Olfactory receptor 2B2 (Olfactory receptor 6-1) (OR6-1) (Hs6M1-10).
GN OR2B2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. AND VARIANT ARG-234.
RA Ziegler A., Ehlers A., Forbes S.A., Trowsdale J., Uchanska-Ziegler B.,
RA Volz A., Younger R., Beck S.;
RT "Polymorphic olfactory receptor genes and HLA loci constitute extended
haplotypes.";
RL (in) Kasahara M. (eds.);
RL Major histocompatibility complex-evolution, structure, and function,
RL pp.110-130, Springer-Verlag, Tokyo (2000).
RN [2]
RP SEQUENCE OF 1-310 FROM N.A.
RA Wild A.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC
DR EMBL; AJ302584; CAC20504.1; -
DR EMBL; AJ302585; CAC20505.1; -
DR

DR EMBL; AJ302586; CAC20506.1; -
DR EMBL; AJ302587; CAC20507.1; -
DR EMBL; AJ302588; CAC20508.1; -
DR EMBL; AJ302589; CAC20509.1; -
DR EMBL; AJ302590; CAC20510.1; -
DR EMBL; AJ302591; CAC20511.1; -
DR EMBL; AJ302592; CAC20512.1; -
DR EMBL; AJ302593; CAC20513.1; -
DR EMBL; 298744; CAB11427.1; -
DR Interpro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction; Polymorphism.
FT DOMAIN 1 25
FT TRANSSEM 26 49
FT DOMAIN 50 57
FT TRANSSEM 58 79
FT DOMAIN 80 100
FT TRANSSEM 101 120
FT DOMAIN 121 139
FT TRANSSEM 140 158
FT DOMAIN 159 195
FT TRANSSEM 196 219
FT DOMAIN 220 236
FT TRANSSEM 237 259
FT DOMAIN 260 272
FT TRANSSEM 273 292
FT DOMAIN 293 357
FT DISULFID 97 189
FT CARBOHYD 5 5
FT VARIANT 234 234
FT
SQ SEQUENCE 357 AA; 40412 MW; 53E2F82820BC440A CRC64;
/FTID=VAR_010943.
/FTID=VAR_010943.
FT
SQ

Query Match
Best Local Similarity 43.8%; Pred. No. 8.2e-45;
Matches 130; Conservative 57; Mismatches 106; Indels 4; Gaps 1;

QY 12 EFVLGGFAPAPARLVLFLLSLDDVVLVTEMLIIAIRNHPFLHKAHPYFLANMSFLEI 71
DB 11 EFVLGVSDQWLEIPFVYMLFISYILFEGNLIILVSHVDEKRLHPRMYFLSLNSLDD 70
QY 72 IWVVTIPKMLAGFISGENHGLISFEACMTQLYFGLGCTECVLLAVAYRYAIC 131
DB 71 LCYTVTPQKLVNMCNTR---KVISYGCVAOLFELFALGSTECILLAVMCFDREVAI 126
QY 132 CHPLHYPIVYSSRLCYVMAAGSMAGGFGISMKVYFLISRLSYCGPNTINHFECVSPILN 191
DB 127 CRPLHYSTIIMHQRICFOLAAASWISGFSNSVSLQSTWTLKMLPCHKEVDFECVPAALK 186
QY 192 LSCDTMSTAEITDFVLAIFILLGLPSVTGASYMATGAVMRIPSAAGHKAFTCSHLTV 251
DB 187 LSCVDITANAELELFISVFLIPVTLILSIYARIVQAVLRIGSAGEGRKAFGCGSHLI 246
QY 252 VTIIFYASIFITYARPKALSAFDTNKLVSIVYAVIPFNPIYICLRNODVYKALRRL 308
DB 247 VSLFYSTAISMYIOPSPSSKDRGKMWLSLFCGIIAPMLNPLITYLRNKEVKEAFKR 303

RESULT 14
O2B2_HUMAN STANDARD; PRT; 312 AA.
ID O2B2_HUMAN
AC O95918;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Olfactory receptor 2H2 (Hs6M1-12).
GN OR2H2.
OS Homo sapiens (Human).
OS

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP NCBI_TaxID=9606;
RA Younger R.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL: AL031983; CAA21455.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 23
FT TRANSMEM 24 47
FT DOMAIN 48 55
FT TRANSMEM 56 77
FT DOMAIN 78 98
FT TRANSMEM 99 118
FT DOMAIN 119 137
FT TRANSMEM 138 156
FT DOMAIN 157 193
FT TRANSMEM 194 217
FT DOMAIN 218 234
FT TRANSMEM 235 257
FT DOMAIN 258 270
FT TRANSMEM 271 290
FT DOMAIN 291 312
FT DISULFID 95 187
FT CARBOHYD 3 3
SQ SEQUENCE 312 AA; 34797 MW; 2C7AB6CCE08A6B6 CRC64;

Query Match 39.7%; Score 669; DB 1; Length 312;
Best Local Similarity 46.6%; Pred. No. 8.6e-45;
Matches 139; Conservative 45; Mismatches 110; Indels 4; Gaps 1;

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O2B6_HUMAN
ID O2B6_HUMAN STANDARD; PRT; 313 AA.
AC P58173; Q9H5B0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Olfactory receptor 2B6 (HS6M1-32) (Olfactory receptor 6-31) (OR6-31).
GN OR2B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Williams S.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL: AL133267; CAC14158.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 25
FT TRANSMEM 26 49
FT DOMAIN 50 57
FT TRANSMEM 58 79
FT DOMAIN 80 100
FT TRANSMEM 101 120
FT DOMAIN 121 139
FT TRANSMEM 140 158
FT DOMAIN 159 195
FT TRANSMEM 196 219
FT DOMAIN 220 236
FT TRANSMEM 237 259
FT DOMAIN 260 272
FT TRANSMEM 273 292
FT DOMAIN 293 313
FT DISULFID 97 189
FT CARBOHYD 5 5
SQ SEQUENCE 313 AA; 35414 MW; 71D459541ACF5301 CRC64;

Query Match 39.5%; Score 667; DB 1; Length 313;
Best Local Similarity 44.1%; Pred. No. 1.2e-44;
Matches 132; Conservative 54; Mismatches 109; Indels 4; Gaps 1;

```

Db 185 LKISCVEFTTANBSELFVSELPHLIP/LTLISYAFIVRAVLRIOSAEGRKAFGTGSH 244
QY 250 LTVVITFEYASTFIYARPKALSAFDNKRKLVSVLYANIVPLFNPIIYCLRNQDVKKALRR 308
Db 245 LIVVSLFYSTAVSVYLQPPSPSSKDOGKMSLEYGIIAPMLNPLIYTLRNKEVKEGFKR 303

Search completed: May 22, 2002, 15:43:55
Job time: 409 sec

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OM protein - protein search, using sw model

Run on: May 22, 2002, 15:31:37 ; Search time 17.62 Seconds
(without alignments)
1783.270 Million cell updates/sec

Title: US-09-771-209-76

Perfect score: 1687
Sequence: 1 MERRNHSGRVSEFVLLGPPA.....RTLHLAODQEAINTKSGKIG 327

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR-71:*
2: PIR1:*
3: PIR3:*
4: PIR4:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1680	99.6	327	2 F23701	olfactory receptor
2	788	46.7	311	2 C23701	olfactory receptor
3	751	44.5	222	2 B40745	odorant receptor (
4	666	39.5	315	2 JC5836	olfactory receptor
5	657.5	39.0	318	2 JC5202	chemoreceptor T864
6	656.5	38.9	313	2 B23701	olfactory receptor
7	650	38.5	316	2 A57069	olfactory receptor
8	644	38.2	312	2 A46247	olfactory receptor
9	642	38.1	305	2 S29711	olfactory factor O
10	636.5	37.7	313	2 S20571	olfactory receptor
11	636	37.7	320	2 S20573	olfactory receptor
12	635	37.6	312	2 A37286	olfactory receptor
13	625	37.0	312	2 I23701	olfactory receptor
14	623.5	37.0	309	1 S51356	olfactory receptor
15	623	36.9	311	2 JC5200	olfactory receptor
16	623	36.9	311	2 S20572	chemoreceptor T833
17	621	36.8	304	2 S29709	olfactory receptor
18	616.5	36.5	314	2 H23701	olfactory receptor
19	616.5	36.5	319	2 JC5624	olfactory receptor
20	613.5	36.4	312	2 A48413	probable olfactory
21	608.5	36.1	307	2 S29710	olfactory receptor
22	607	36.0	315	2 JC4658	olfactory receptor
23	606.5	36.0	333	2 A23701	olfactory receptor
24	605.5	35.9	314	2 S29707	olfactory receptor
25	605	35.9	317	2 D23701	olfactory receptor
26	600	35.6	312	2 S29708	olfactory receptor
27	587	34.8	310	2 E23701	olfactory receptor
28	573	34.0	315	2 JC5201	chemoreceptor T856
29	570	33.8	312	2 JC23701	olfactory receptor

30	524	31.1	312	2 A46750	olfactory receptor
31	500.5	29.7	264	2 PC4369	olfactory receptor
32	467	27.7	222	2 D40745	odorant receptor (
33	451	26.7	234	2 S29000	G protein-coupled
34	449	26.6	216	2 I38480	olfactory receptor
35	445	26.4	232	2 S29001	G protein-coupled
36	440	26.1	216	2 I38481	olfactory receptor
37	438.5	26.0	328	2 G45774	odorant receptor 2
38	431	25.5	216	2 I38479	olfactory receptor
39	431	25.5	234	2 S28998	G protein-coupled
40	430	25.5	216	2 I38474	olfactory receptor
41	426.5	25.3	225	2 I38478	olfactory receptor
42	424	25.1	216	2 I38470	olfactory receptor
43	423	25.1	216	2 I38476	olfactory receptor
44	421.5	25.0	215	2 I38473	olfactory receptor
45	410	24.3	222	2 C40745	odorant receptor (

ALIGNMENTS

RESULT 1
F23701
olfactory receptor I7 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C:Accession: F23701
R:Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A:Title: A novel multigene family may encode odorant receptors: a molecular basis for
A:Reference number: A23701; MUID:91191556
A:Accession: F23701
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-327 <BUC>
A:Cross-references: GB:M64386; NID:g205833; PIDN:AAA41749.1; PID:g205834
C:Superfamily: olfactory receptor OR14
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 99.6%; Score 1680; DB 2; Length 327;
Best Local Similarity 99.7%; Pred. No. 1.2e-140;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MERRNHSGRVSEFVLLGPPAPAPRLVLLPFLSLDYVLTENMLITAIRNHPPLHKPM	60
DB	1	MERRNHSGRVSEFVLLGPPAPAPRLVLLPFLSLDYVLTENMLITAIRNHPPLHKPM	60
QY	61	YFELANMSFLEIWTYVTVIPKMLAGFISKENHGOLISFEACMTQLYFELGIGCTECVLL	120
DB	61	YFELANMSFLEIWTYVTVIPKMLAGFISKENHGOLISFEACMTQLYFELGIGCTECVLL	120
QY	121	AVMAIDRYVAICHPLHRYVYYSRLCYOMAGSNAGGGSISWVKFLISRLSYCGPNTIN	180
DB	121	AVMAIDRYVAICHPLHRYVYYSRLCYOMAGSNAGGGSISWVKFLISRLSYCGPNTIN	180
QY	181	HFPCVSPFLNLSCTDMSTAEITDFVLAIFITLGLPSTVGASYSMTAGVAMRIPSAAGR	240
DB	181	HFPCVSPFLNLSCTDMSTAEITDFVLAIFITLGLPSTVGASYSMTAGVAMRIPSAAGR	240
QY	241	KAFTSCASHLVTVIIFVAASIFIVARPKALSAFTDNKLVSULYAVIVLPNDIIVCLRNQ	300
DB	241	KAFTSCASHLVTVIIFVAASIFIVARPKALSAFTDNKLVSULYAVIVLPNDIIVCLRNQ	300
QY	301	DVKRALRRTLHLAODQEAINTKSGKIG 327	
DB	301	DVKRALRRTLHLAODQEAINTKSGKIG 327	

RESULT 2
C23701
olfactory receptor F6 - rat
C:Species: Rattus norvegicus (Norway rat)

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
 C:Accession: C23701
 R:Buck, L.; Axel, R.
 Cell 65, 175-187, 1991
 A>Title: A novel multigene family may encode odorant receptors: a molecular basis for od
 A:Reference number: A23701; M0ID:91191556
 A:Accession: C23701
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-311 <BU>
 A:Cross-references: GB:M64378; NID:9205817; PIDN:AAA1741.1; PID:9205818
 C:Superfamily: olfactory receptor OR14
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 46.7%; Score 788; DB 2; Length 311;
 Best Local Similarity 50.7%; Pred. No. 5,4e-62;
 Matches 151; Conservative 46; Mismatches 97; Indels 4; Gaps 1;

QY 13 FVLGFPAPAPRLVLFLLSLDYLVLTEMLIIAIRNHPYLRKPMYFFLANMSFLEI 72
 D 15 FILGFPGRSMRIGLFLFLVYLLTVGNLAIISLVGHRCLQTPMVEFLCNLSFLEI 74
 QY 73 WYTVYIPKMLAGFISCKENHGLISFEACMTQLYFFLGCTEYLLAMAYDRYVAIC 132
 D 75 WFTTACVPTLATF---APRGVISLACGATQMYEVSIGCTEYFLAMAYDRYLAIC 130
 QY 133 HPLHYVYIYSSRLCYOMAGSNGFGISVMYKVFELISLTCGPNITNHFCEVPLNLT 192
 D 131 LPLRTGIMTGLMLALGSLGCSALTVPRTLARISECSRYINHFCEISPMIVL 190
 QY 193 SCTDMSTAEITDFVLAIFLLGPLSVTGASYMAITGAVMRIPSAGRKAKSTCASHLYV 252
 D 191 SCTDQVEELVSFGIAFCVILGSCGITLVSAVYIITFIIRKIPARGHRASFSSHLTV 250
 QY 253 VILFFVASTFIYARPKALSAFDTNKLVSYLXATVPLFNITICLNODYKRALRRTL 310
 D 251 VLIWGTSTFLHVRISVESLDTKATVLTNTVPLNPEIYTLNRKDKVEALRRTV 308

RESULT 3

BA0745
 odorant receptor (clone K18) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
 C:Accession: BA0745
 R:Resler, K.J.; Sullivan, S.L.; Buck, L.B.
 Cell 73, 597-609, 1993
 A>Title: A zonal organization of odorant receptor gene expression in the olfactory epith
 A:Reference number: A40745; M0ID:93258822
 A:Accession: BA0745
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-222 <RES>
 A:Cross-references: GB:L14567; NID:9293755; PIDN:AAA39861.1; PID:9293756
 A:Experimental source: olfactory epithelium
 A>Note: sequence extracted from NCBI backbone (NCBIP:131748)
 C:Superfamily: olfactory receptor OR14
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 44.5%; Score 751; DB 2; Length 222;
 Best Local Similarity 61.2%; Pred. No. 7e-59;
 Matches 137; Conservative 36; Mismatches 47; Indels 4; Gaps 1;

QY 62 FFLANMSFLEIYVYITIKMLAGFISCKENHGLISFEACMTQLYFFLGCTEYLLA 121
 D 1 YFLSTMSFLEAMTISTYVTKMLAGL---FHPNTISFLGCMQLYFFLSLACTEYLLA 56
 QY 122 WYABRYVAVICHLHPYVYIYSSRLCYOMAGSNGFGISVMYKVFELISLTCGPNITN 181
 D 57 AAAYDRYVAVICHLHPYVYIYSSRLCYOMAGSNGFGISVMYKVFELISLTCGPNITN 116

QY 182 FCDVSPFLNLSCTDMSTAEITDFVLAIFLLGPLSVTGASYMAITGAVMRIPSAGRK 241
 D 117 FCDVSPILTLACNMNLSMATVDFALAVILIFPLSATVLSGYSTVQIPSATGQRK 176
 QY 242 AFSTCASHLTIVVIFVYASIFITARPKALSAFDTNKLVSYLXAV 285
 D 177 AFSTCASHLTIVVIFVYAVIFMYRPRALASFNSNKLISAIVAV 220

RESULT 4

JC5836
 olfactory receptor-like protein 2 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 24-Nov-1999
 C:Accession: JC5836
 R:Blache, P.; Gros, L.; Salazar, G.; Bataille, D.
 Blochem. Biophys. Res. Commun. 242, 669-672, 1998
 A>Title: Cloning and tissue distribution of a new rat olfactory receptor-like (OL2).
 A:Reference number: JC5836; M0ID:98125551
 A:Accession: JC5836
 A>Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-315 <BLA>
 A:Cross-references: GB:AF029337; NID:92570934; PIDN:AAC39969.1; PID:92570935
 C:Comment: This protein is implicated in white cell muturation and migration.
 C:Superfamily: olfactory receptor OR14
 F:28-53/Domain: transmembrane #status predicted <TM1>
 F:46-66/Domain: transmembrane #status predicted <TM2>
 F:95-123/Domain: transmembrane #status predicted <TM3>
 F:147-165/Domain: transmembrane #status predicted <TM4>
 F:203-229/Domain: transmembrane #status predicted <TM5>
 F:241-264/Domain: transmembrane #status predicted <TM6>
 F:277-293/Domain: transmembrane #status predicted <TM7>

Query Match 39.5%; Score 666; DB 2; Length 315;
 Best Local Similarity 43.8%; Pred. No. 3.2e-51;
 Matches 135; Conservative 59; Mismatches 110; Indels 4; Gaps 1;

QY 3 RRNHSGRVSEFVLLGFPAPAPRLVLFLLSLDYLVLTEMLIIAIRNHPYLRKPMY 62
 D 5 RKENCSSVSEFILLGRSSSEQIRMALEFIFLLYKWTLLNGLVALITYDSRLRHPMY 64
 QY 63 FLANMSFLEIYVYITIKMLAGFISCKENHGLISFEACMTQLYFFLGCTEYLLAV 122
 D 65 FLTSLSDVMSYVTVTPQQLVMNVCPK---RTISMGACVAMFIFVLGIACVLYAI 120
 QY 123 MAYDRYVAVICHLHPYVYIYSSRLCYOMAGSNGFGISVMYKVFELISLTCGPNITN 182
 D 121 MAYDRYVAVICHLHPYVYIYSSRLCYOMAGSNGFGISVMYKVFELISLTCGPNITN 180
 QY 183 FCDVSPFLNLSCTDMSTAEITDFVLAIFLLGPLSVTGASYMAITGAVMRIPSAGRK 242
 D 181 FCEVPAVLKACADTSNDLDFILGFLVLLVPLSLASACIFISILIRSSQGRKLS 240
 QY 243 FSTCASHLTIVVIFVYASIFITARPKALSAFDTNKLVSYLXAVIPLFNITICLNODY 302
 D 241 FSTCASHLTIVVIFVYAVIFMYRPRALASFNSNKLISAIVAVIPLFNITICLNODY 300
 QY 303 KRALRRTL 310
 D 301 KGAFMRVL 308

RESULT 5

JC5202
 chemoreceptor TB641 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 20-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-Aug-1999
 C:Accession: JC5202; PC4304
 R:Thomas, M.B.; Haines, S.L.; Akesson, R.A.
 Gene 178, 1-5, 1996
 A>Title: Chemoreceptors expressed in taste, olfactory and male reproductive tissues.

A:Reference number: JCS200; MUID:97080538
A:Accession: JCS202
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-318 <TH01>
A:Cross-references: GB:U0949; NID:g1256392; PIDN:AAC52911.1; PID:g1256393
A:Accession: PC4304
A:Status: preliminary
A:Molecule type: protein
A:Residues: 145-153; 245-253 <TH02>
A:Experimental source: taste bud
C:Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction
C:Genetics:
A:Gene: tb641
C:Superfamily: olfactory receptor OR14
C:Keywords: olfaction; taste bud; transmembrane protein
F:30-53/Domain: transmembrane #status predicted <TM1>
F:63-84/Domain: transmembrane #status predicted <TM2>
F:106-125/Domain: transmembrane #status predicted <TM3>
F:145-169/Domain: transmembrane #status predicted <TM4>
F:202-224/Domain: transmembrane #status predicted <TM5>
F:243-265/Domain: transmembrane #status predicted <TM6>
F:276-286/Domain: transmembrane #status predicted <TM7>

Query Match	39.0%	Score 657.5;	DB 2;	Length 318;
Best Local Similarity	42.3%	Pred. No. 1.8e-50;		
Matches 135; Conservative	56;	Mismatches 101;	Indels 27;	Gaps 6;

[illegible]

RESULT 6
B23701
Olfactory receptor F5 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 04-Sep-1998
C:Accession: B23701
R:Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A:Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A:Reference number: A23701; MUID:91191556
A:Accession: B23701
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-313 <BUC>
A:Cross-references: GB:M64377
C:Superfamily: Olfactory receptor OR14
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	38.98;	Score 656.5;	DB 2;	Length 313;
Best Local Similarity	44.18;	Pred. No. 2.2e-50;		
Matches 137;	Conservative 50;	Mismatches 117;	Indels 7;	Gaps

```

QY      1 MERNHSGRSEVFLLEFPAPAPRLRYVLFPLSLDVLVTEMLLILRNHPYLHKRM 60
Db      1 MSLSTNOSS-VTEFLLELILSKPOOOOLLFLLELIMTALVGLNLIITLIGDSDRLHPM 59

QY      61 YEFLLANNSFLEIMVYVTVTIKMLAGFI-GSKENHGOLISFEACMOLYFELIAGCTEVL 119
Db      60 YEFLLNLSLSPVDVCSSTTVPKVLNHHLS-----QAISFGSLQLQVLYLAFGMDNDFL 114

QY      120 LAVNAYDHYVAICHPLHYPIYVSSRLCVQMAAGSMAGFGGISIMKVKELISRLSYCGPMT 179
Db      115 LAVSYDHFVAICHPLHYTTKMTROLCEVLLLVGSMVYVANNCLLHLLIMARKSPCADNMI 174

QY      180 NHFCVDYSPLLNLSTGTMSTAEITDEVLAFILILGELSTGASYAIIITGAIVKRIFSAAGR 239
Db      175 PHFCFSTGTPLLKLSGDSPTHTNELMILTEGAVVYVTPFCVILISYIHITCAVLRVSSPRGG 234

QY      240 HKARSTQASHLTIVIIIFYAASIFIYARPKALSAFDINKLVSYLYANIVPLFMDPIIYCRN 299
Db      235 WKSSSTGSGSHLAAVVCIFYGVIAVENPSSSHLAGRDMAAAVYAVVTPMLNPFIYSLRN 294

QY      300 QDVYKRALRRTL 310
Db      295 SDMKALLRKYL 305

```

RESULT 7
A57069
olfactory receptor FAT11 - human
C:Species: Homo sapiens (man)
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 26-Aug-1999
C:Accession: A57069
R:Pan, W.; Liu, Y.C.; Parimoo, S.; Weissman, S.M.
Genomics 27, 119-123, 1995
A:Title: Olfactory receptor-like genes are located in the human major histocompabil
A:Reference number: A57069; MUID:95394447
A:Accession: A57069
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-316 <FAN>
A:Cross-references: GB:J35475; NID:g1041044; PIDN:AAB36567.1; PTD:g601919
C:Genetics:
A:Gene: GDB:FAT11; OLFR2
A:Cross-references: GDB:1323249; OMIM:600578
A:Map position: 6p21.3-6p21.3
C:Superfamily: olfactory receptor OR14

Query Match	38.5%	Score 650;	DB 2;	Length 316;
Best Local Similarity	45.2%;	Pred. NO. 8.2e-50;		
Matches 137;	Conservative 48;	Mismatches 114;	Indels 4;	Gaps 1;

[illegible]

Db 246 VTLFYSSVAVIYIQPKNPYAQGRKFGFLYAVGTPSLNPLVYTLRNKEIKRALRLLG 305
OY 313 AOD 315
Db 306 ERD 308

RESULT 8
A46247
Olfactory receptor OR3 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
C:Accession: A46247
R:Neif, P.; Hermans-Borgmeyer, I.; Artieres-Pin, H.; Beasley, L.; Dionne, V.E.; Heinemann
Proc. Natl. Acad. Sci. U.S.A. 89, 8948-8952, 1992
A:Title: Spatial pattern of receptor expression in the olfactory epithelium.
A:Reference number: A46247; MUID:93028384
A:Accession: A46247
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-312 <MEF>
A:Cross-references: GB:M84005; NID:g200153; PIDN:AAA39862.1; PID:g200154
A:Note: sequence extracted from NCBI backbone (NCBIP:115362)
C:Superfamily: olfactory receptor OR14

Query Match 38.2%; Score 644; DB 2; Length 312;
Best Local Similarity 43.0%; Pred. No. 2,7e-49;
Matches 128; Conservative 55; Mismatches 111; Indels 4; Gaps 1;

OY 13 FVLGGPAPAPRVLFSLSDIVLVLTENMLIIRNHPYLHKPFFLANMSFLEI 72
Db 12 FILMGVSDHPHLIIFFAVILASVLTLVGNLIIILSRDARLHPMYEFLSLSL 71
OY 73 WYVVTIPKMLAGFISKENHGOLISPEACMTQLYFLGCTECVLLAVMAYDRYVAIC 132
Db 72 AFTTSSVPQMLKMLMGPDRTK----ISYGCCTQLYVFLMGATECILLVYMAEDRYAVC 127
OY 133 HPLHYPIVYSSRLCYOMAGSMAGGFGISMKVYKVLISRLSYCGPNTINHPFCDSVPLNT 192
Db 128 RPLHYMTVMNPRLCWLGLAISMLGSLGNSVYIGSTFTQLPFCGHRKVDNLCFEPAMIKL 187
OY 193 SCIDMSTAEITDVLAFILILGPLSVTGASYMATGAVMRIPSAAGHKAFTSCASHLV 252
Db 188 ACGDSTLNEVLNGVCFEFTVPVSVILVSYCFIAQVAMIRSEGRKKAFCVSHLV 247
OY 253 VILFYASIFIVARPKALSAFDTNKLVSVYAVIVLPFNPIIYCLRNQDVKRALRLRT 310
Db 248 VLFYGSATIGYLLPAKSSNQSGKFIISLYSVTPRVNPLIYTLRKKEVGKALGRLL 305

RESULT 9
S29711
Olfactory factor OR37 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
C:Accession: S29711
R:Ramming, K.; Krieger, J.; Strotmann, J.; Boehkoff, I.; Kubick, S.; Baumstark, C.; Breech
Nature 361, 353-356, 1993
A:Title: Cloning and expression of odorant receptors.
A:Reference number: S29707; MUID:93149273
A:Accession: S29711
A:Molecule type: mRNA
A:Residues: 1-305 <RAM>
C:Superfamily: olfactory receptor OR14

Query Match 38.1%; Score 642; DB 2; Length 305;
Best Local Similarity 43.9%; Pred. No. 4e-49;
Matches 133; Conservative 57; Mismatches 103; Indels 10; Gaps 3;

OY 14 VILGFPAPAPRVLFSLSDIVLVLTENMLIIRNHPYLHKPFFLANMSFLEI 73
Db 13 VILGFPAPAPRVLFSLSDIVLVLTENMLIIRNHPYLHKPFFLANMSFLEI 73

Db 1 LLLGSGPYKTEILYEVIVLVYVLIHTGNGVLIITASIPDSHLTPMYFFLGNI-SFLDIC 60
OY 74 YVTVTIKMLAGFISKENHGOLISPEACMTQLYFLGCTECVLLAVMAYDRYVAIC 133
Db 61 YTTSSVPSTVLSLKKRN-----ISFGCTVQMGVGRFAMSGTECLLGNMAFDYVAICN 116
OY 134 PLHYPIVYSSRLCYOMAGSMAGGFGISMKVYKVLISRLSYCGPNTINHPFCDSVPLNTLS 193
Db 117 PLRYSVIMSKREYVYMASASWFSGINSVQTSILAMRLPFCGNVNIHNFCEVAIVLKL 176
OY 194 CTDMSTAEITDVLAFILILGPLSVTGASYMATGAVMRIPSAAGHKAFTSCASHLV 253
Db 177 CADISLNIWTVISNMALVPLVPLLIFFSTVLIYTLIRNMSASGRKRAFSTCSAHLTV 236
OY 254 IIFYASIFIVARPKA--LSAFD----TNKLVSVYAVIVLPFNPIIYCLRNQDVKRALR 307
Db 237 VIEGTIFSMYAKPKSQDLGKDFQTSIDKRIISLFYGVVPMPLPIIYSLRNKVKAAVK 296
OY 308 RTL 310
Db 297 YIL 299

RESULT 10
S20571
Olfactory receptor - dog
C:Species: Canis lupus familiaris (dog)
C>Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 26-Aug-1999
C:Accession: S20571
R:Parmentier, M.; Libert, F.; Schirrans, S.; Schiffrmann, S.; Lefort, A.; Eggerickx, D
Nature 355, 453-455, 1992
A:Title: Expression of members of the putative olfactory receptor gene family in mamm
A:Reference number: S20571; MUID:92131132
A:Accession: S20571
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-313 <PAR>
A:Cross-references: EMBL:X64996; NID:g890; PIDN:CAA46129.1; PID:g891
C:Superfamily: olfactory receptor OR14
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 37.7%; Score 636.5; DB 2; Length 313;
Best Local Similarity 43.2%; Pred. No. 1.3e-48;
Matches 130; Conservative 55; Mismatches 111; Indels 5; Gaps 2;

OY 10 VSEFVLGFPAPAPRVLFSLSDIVLVLTENMLIIRNHPYLHKPFFLANMSF 69
Db 9 VSEFVLGFLTDPDQRLFYALFLAMVYTIILGMLIIVLIQDSHLHTPMYFLSLMSF 68
OY 70 LEIYVTVTIKMLAGFISKENHGOLISPEACMTQLYFLGCTECVLLAVMAYDRYV 129
Db 69 SDLCFSSVTMPKLLQ---NMQSQVPSIPYAGCLTQMYFLFPGDLSPLLVAMAYDRYV 124
OY 130 ALCHPLHYPIVYSSRLCYOMAGSMAGGFGISMKVYKVLISRLSYCGPNTINHPFCDSVPL 189
Db 125 ALCEPLHYTTIMSPKLCFSLVLSWVLTMPHVAVHTLMLARLCECA-NLTPHPFCDSAL 183
OY 190 LINSCTMSTAEITDVLAFILILGPLSVTGASYMATGAVMRIPSAAGHKAFTSCASH 249
Db 184 LKACSTQVNELVIFIMGLIIVIPFLIITTSARIVSSILKVPASIGICKFVSTCGSH 243
OY 250 LTVVLIIFYASIFIVARPKALSAFDTNKLVSVYAVIVLPFNPIIYCLRNQDVKRALRLRT 309
Db 244 LSVVSLFYGVIGLYCLPSANNSYVKETINAMMYTVTPPLNPIYSLRNKDKKALGRV 303
OY 310 L 310
Db 304 I 304

RESULT 11
S20573

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Query Match Similarity      37.6% Score 635 DB 2 Length 314;
Best Local Similarity       41.9% Pred. NO. 1.7e-48;
Matches 126 Conservative    59 Mismatches 112 Indels   4 Gaps   1;

Qy 10 VSEVVLGGPAPAPLRLFLFTSLDDYLVLTENMLIIATIRNHPPLAKPMVEFLANNSF 69
     ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
db 9 ISQIFLLPIRSEHQHFVALFSMTYGLTVVGNIILHLHDSHLLHTPMFLPFSSNF 68

```

RESULT 14
S51356
olfactory receptor - rat
C:Species: Rattus norvegicus (Norway rat)

Query Match	37.0%;	Score 623.5;	DB 1;	Length 309;
Best Local Similarity	42.8%;	Pred. No. 1.7e-47;		
Matches 130; Conservative	56;	Mismatches 113;	Indels 5;	Gaps 2

RESULT 15
JC5200

Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction

Query Match	36.9%	Score 623;	DB 2;	Length 311;
Best Local Similarity	43.1%	Pred. No. 1.9e-47;		
Matches 131;	Conservative 54;	Mismatches 109;	Indels 10;	Gaps 3

Db 300 KRL 303

Job time: 547 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 22, 2002, 15:30:55 ; Search time 13.05 Seconds
(without alignments)
612.044 Million cell updates/sec

Title: US-09-771-209-76

Perfect score: 1687

Sequence: 1 MERRNHSGRSEFVLLGPPA.....RTLLADQDEANTNGSKIG 327

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:.*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1382.5	82.0	286	1	US-08-118-270-65
2	1382.5	82.0	286	5	PCT-US93-08528-65
3	705	41.8	277	1	US-08-118-270-62
4	705	41.8	277	5	PCT-US93-08528-62
5	666	39.6	321	4	US-08-748-506-18
6	666	39.6	321	4	US-08-748-506-10
7	660	39.1	321	4	US-08-748-506-20
8	658	39.0	321	4	US-08-748-506-11
9	658	39.0	321	4	US-08-748-506-12
10	654	38.8	321	4	US-08-748-506-19
11	653	38.7	321	4	US-08-748-506-13
12	633.5	37.6	327	4	US-08-748-506-24
13	623.5	37.0	327	4	US-08-748-506-14
14	623	36.9	314	3	US-08-988-876-7
15	616	36.5	327	4	US-08-748-506-22
16	616	36.5	327	4	US-08-748-506-23
17	614.5	36.4	309	3	US-08-988-876-5
18	607	36.0	284	1	US-08-118-270-61
19	607	36.0	284	5	PCT-US93-08528-61
20	606.5	35.5	333	3	US-08-988-876-6
21	599	35.5	316	2	US-08-827-291A-2
22	575.5	34.1	296	2	US-08-467-948A-2
23	575.5	34.1	296	3	US-08-467-947A-2
24	524.5	31.1	293	1	US-08-118-270-60
25	524.5	31.1	293	5	PCT-US93-08528-60
26	517.5	30.7	274	1	US-08-118-270-69
27	517.5	30.7	274	5	PCT-US93-08528-69

28	514	30.5	247	1	US-08-465-980-3	Sequence 3, App1
29	514	30.5	247	2	US-09-053-303-3	Sequence 3, App1
30	514	30.5	247	5	PCT-US95-07093-3	Sequence 3, App1
31	513.5	30.4	284	1	US-08-118-270-67	Sequence 67, App1
32	513.5	30.4	284	5	PCT-US93-08528-67	Sequence 67, App1
33	506	30.0	100	4	US-09-085-371-6	Sequence 67, App1
34	498.5	29.5	277	1	US-08-118-270-68	Sequence 68, App1
35	498.5	29.5	277	5	PCT-US93-08528-68	Sequence 68, App1
36	496	29.4	273	1	US-08-118-270-63	Sequence 63, App1
37	496	29.4	273	5	PCT-US93-08528-63	Sequence 63, App1
38	467	27.7	222	2	US-08-467-948A-27	Sequence 27, App1
39	467	27.7	222	3	US-08-467-947A-27	Sequence 27, App1
40	456	27.0	275	1	US-08-118-270-66	Sequence 66, App1
41	456	27.0	275	5	PCT-US93-08528-66	Sequence 66, App1
42	437	25.9	269	1	US-08-118-270-64	Sequence 64, App1
43	437	25.9	269	5	PCT-US93-08528-64	Sequence 64, App1
44	407	24.1	320	4	US-09-439-113-527	Sequence 527, App
45	396	23.5	320	1	US-08-465-980-2	Sequence 2, App1

ALIGNMENTS

RESULT 1

US-08-118-270-65

Sequence 65, Application US/08118270

Patent No. 5508384

GENERAL INFORMATION:

APPLICANT: Murphy, Randall B.

APPLICANT: Schuster, David I.

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

NUMBER OF SEQUENCES: 348

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEWMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/118,270

FILING DATE: 09-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, Kevin G.

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MURPHY-2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-118-270-65

Query Match

Best Local Similarity

Matches 276; Conservative

Score 1382.5; DB 1; Length 286;

Pred. No. 3,5e-116;

Mismatches 6;

Indels 15;

Gaps 4;

OY 27 LFFLSLDIVLVLTENMLIIIRNHPPLHKPMYFFLANMSFLEIWTYVTITPKMLAGF 86
|||||
Db 1 LFFLSLDIVLVLTENMLIIIRNHPPLHKPMYFFL-----FLEIWTYVTITPKLM-GF 55
OY 87 IGSKENHGOLISFEACMTQLYFFLGCTECVCLLAWANDRYVAICHPHYPIYVSSRLC 146
|||||
Db 56 IGSKENHGOLISFEACMTQLYFFLGCTECVCLLAWANDRYVAICHPHYPIYVSSRLC 115
OY 147 VQMAAGSMAGGFGISWVKVFLISRLSYCGPNTINHFECVSPPLNLSCTDMSTAELTDFV 206
| |||||
Db 116 V---LGSWAGGFGISWVKVFLISRLSYCGPNTINHFECVSPPLNLSCTDMSTAELTDFV 172
OY 207 LAIFILGLPLSTGASYMAITGAVMRIPSAAGRHKAFSTCASHLVYIIIFYAASITTYAR 266
: |||||
Db 173 LAIFILGLPLSTGASY-----MRIPSAAGRHKAFSTCASHLVYIIIFYAASITTYAR 225
OY 267 PKALSAFDNKLVSIVYAVIVPLFNPIITCLRNQDVKRALRRTLHLAODEANTNGSKSI 326
| |||||
Db 226 PKALSAFDNKLVSIVYAVIVPLFNPIITCLRNQDVKRALRRTLHLAODEANTNGSKSI 285
OY 327 G 327
|
Db 286 G 286

RESULT 2
PCT-US93-08528-65
; Sequence 65, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-08528-65

Query Match 82.0%; Score 1382.5; DB 5; Length 286;
Best Local Similarity 91.7%; Pred. No. 3.5e-116;
Matches 276; Conservative 4; Mismatches 6; Indels 15; Gaps 4;

OY 27 LFFLSLDIVLVLTENMLIIIRNHPPLHKPMYFFLANMSFLEIWTYVTITPKMLAGF 86
|||||
Db 1 LFFLSLDIVLVLTENMLIIIRNHPPLHKPMYFFL-----FLEIWTYVTITPKLM-GF 55
OY 87 IGSKENHGOLISFEACMTQLYFFLGCTECVCLLAWANDRYVAICHPHYPIYVSSRLC 146
|||||
Db 56 IGSKENHGOLISFEACMTQLYFFLGCTECVCLLAWANDRYVAICHPHYPIYVSSRLC 115
OY 147 VQMAAGSMAGGFGISWVKVFLISRLSYCGPNTINHFECVSPPLNLSCTDMSTAELTDFV 206
| |||||
Db 116 V---LGSWAGGFGISWVKVFLISRLSYCGPNTINHFECVSPPLNLSCTDMSTAELTDFV 172
OY 207 LAIFILGLPLSTGASYMAITGAVMRIPSAAGRHKAFSTCASHLVYIIIFYAASITTYAR 266
: |||||
Db 173 LAIFILGLPLSTGASY-----MRIPSAAGRHKAFSTCASHLVYIIIFYAASITTYAR 225
OY 267 PKALSAFDNKLVSIVYAVIVPLFNPIITCLRNQDVKRALRRTLHLAODEANTNGSKSI 326
| |||||
Db 226 PKALSAFDNKLVSIVYAVIVPLFNPIITCLRNQDVKRALRRTLHLAODEANTNGSKSI 285
OY 327 G 327
|
Db 286 G 286

RESULT 3
US-08-118-270-62
; Sequence 62, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-118-270-62

Query Match 41.8%; Score 705; DB 1; Length 277;
Best Local Similarity 49.7%; Pred. No. 1.2e-55;

[illegible]

```

: RESULT 4
: PCT-US93-08528-62
: Sequence 62, Application PC/TUS9308528
: GENERAL INFORMATION:
: APPLICANT: New York University
: TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
: NUMBER OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
: NUMBER OF SEQUENCES: 348
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEWMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/08528
: FILING DATE: 09-SEP-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/943,236
: FILING DATE: 10-SEP-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Townsend, Kevin G.
: REGISTRATION NUMBER: 34,033
: REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: TELEX: 248633
: INFORMATION FOR SEQ ID NO: 62:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 277 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: PCT-US93-08528-62

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Query Match	41.8%	Score 705	DB 5	Length 277
Best Local Similarity	49.7%	Pred. No. 1.2e-55		
Matches 142	Conservative 41	Mismatches 89	Indels 14	Gaps 4
OY	27	LLEFLSLDDYVVLVENNMIIAIIINHPIL--HKPMYFFLAMSFLIEIYVYVTVIIPKMLA-84		

Db 1 LPLFLFLVWYLLVTVGNLAIIISLVGAHRCIQPHRPMVFLICNLSFLEIMFTTACVPRTLA 60
 QY 85 GFISGKHNHQLISFEACMTQLYFFLGICTECVLLAVMAIDRYVAICHPLHRYVYSSR 144
 Db 61 TF----AERGAVISLAGCATI-YEVFSGICTEEYVLLAVMADRLLACLPLRYGIMRPG 115
 QY 145 LCYQMAAGSNAGMGFGISWVKVFLLSRLSYCGCPNFINAFECVSPFLNISCSDMSIAETLD 204
 Db 116 IAMRALASWMLCGSATIYPTALLRLARSFCGSKRIINHFPCDISWLYISCTDIOVELYS 175
 QY 205 FVLALFILLGPLSVTGSYMAITGAVMRIPSRARHKAFSTCASHLTIVIIFFAASIFIIY 264
 Db 176 FGIAFCVLLGSCGIIIVSY-----AKIPARBRHRAFSCTSHLTIVLIWGSTIFLH 228
 QY 265 ARPKALSFEDNKLVSIVYAVIVLPNFIICLLENOYKRLARITL 310
 Db 229 VRTISESSLDLTKAITYLNTIVTVFVLPNFIITLNNKYKELKRTIV 274

```

RESULT 5
US-08-748-506-18
: Sequence 18, Application US/08748506
: Patent No. 6139707
:
: GENERAL INFORMATION:
: APPLICANT: Ronnett et al.
: TITLE OF INVENTION: NOVEL SPERM RECEPTORS
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Leydig, Volt & Mayer, Ltd.
: STREET: Two Prudential Plaza, Suite 4900
: CITY: Chicago
: STATE: IL
: COUNTRY: US
: ZIP: 60601-6780
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/748,506
: FILING DATE: 08-NOV-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/033,751
: FILING DATE: 09-NOV-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: REFERENCE/DOCKET NUMBER: 74940
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5600
: TELEFAX: 312-616-5700
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 321 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
US-08-748-506-18

```

	Query Match	39.6%	Score 668;	DB 4;	Length 321;	
	Best Local Similarity	47.6%;	Pred. No. 2.8e-52;			
	Matches 136; Conservative	47;	Mismatches 99;	Indels	4;	Gaps 1.
Oy	27	LLEFLSLDYVYLVEENMLIIITATNNHPILKPMYEPFLANSELEIKWVTYTPIMKLAGE	86			
Db	32	LLEFLILMLFVLSTGLNTLIVLAICTSPSLRPMYFPLANLSLLEIGYCVPYMKLOSL	91			
Oy	87	IGSKENHGOLISFEACMQLVFYELGCTECYLLAVMAVDRAVCPLHYPVIAYSSRC	146			
Db	92	V-----SEKRETISRCCATQMFEEFAFGITECCLLANAMAFDRCMALICSPHYATRRSREV	147			

ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-748-506-19

Query Match 38.8%; Score 654; DB 4; Length 321;
Best Local Similarity 46.8%; Pred. No. 5e-51;
Matches 137; Conservative 42; Mismatches 110; Indels 4; Gaps 1;

QY 27 LLEFLSLDYLVLVTENMLIIIRNHPILHKPMYFFLANMSFLEIYVTVTPKMLAGF 86
DB 32 LLEFLSLDYLVLVTENMLIIIRNHPILHKPMYFFLANMSFLEIYVTVTPKMLAGF 91
QY 87 IGSKENHGOISFEACMTQYFELGCTCEVLLAVMADRYVAICHPHYPIVSRIC 146
DB 92 V-----SEARISREGCATQWFFFTFGITCCCLLAAMAFDRYMAICSPHYATRMSREVC 147
QY 147 VQMAAGSMAGFCGISWVKYFELISRLSYCGPNTINHFCDVSPLLNCTDMSTAELTDFV 206
DB 148 AHLAIYSWMGCIYGLGQTNIIISLNFCCGCEIDHFCDDPLALACDTSQNEAIFV 207
QY 207 LAIFILLGPLSVTGASYMAITGAVMRIPSAGRHKAFTSCASHLYVIIIFYASITFYAR 266
DB 208 AAFLICSSPFLVLYSVIRLVAVLWVPSBEGHKKALSTCSSHLVLTLYFGSGSVTYLR 267
QY 267 PKALSAFDNTKLVSYLAVIVPLFNPIIYCLRNODVKRALRRLTLHADOQEAN 319
DB 268 PKSSHSPGMDKLALFLTYAVTSMLNPIIYSLRNKDYKALRLTLHADOQEAN 320

RESULT 11
US-08-748-506-13
Sequence 13, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-748-506-13

Query Match 38.7%; Score 653; DB 4; Length 321;
Best Local Similarity 46.5%; Pred. No. 6.1e-51;
Matches 133; Conservative 43; Mismatches 106; Indels 4; Gaps 1;

QY 27 LLEFLSLDYLVLVTENMLIIIRNHPILHKPMYFFLANMSFLEIYVTVTPKMLAGF 86
DB 32 LLEFLSLDYLVLVTENMLIIIRNHPILHKPMYFFLANMSFLEIYVTVTPKMLAGF 91
QY 87 IGSKENHGOISFEACMTQYFELGCTCEVLLAVMADRYVAICHPHYPIVSRIC 146
DB 92 VSEAREIFV---GCATQWFFFTFGITCCCLLAAMAFDRYMAICSPHYATRMSREVC 147
QY 147 VQMAAGSMAGFCGISWVKYFELISRLSYCGPNTINHFCDVSPLLNCTDMSTAELTDFV 206
DB 148 AHLAIYSWMGCIYGLGQTNIIISLNFCCGCEIDHFCDDPLALACDTSQNEAIFV 207
QY 207 LAIFILLGPLSVTGASYMAITGAVMRIPSAGRHKAFTSCASHLYVIIIFYASITFYAR 266
DB 208 VVVLICSSPFLVLYSVIRLVAVLWVPSBEGHKKALSTCSSHLVLTLYFGSGSVTYLR 267
QY 267 PKALSAFDNTKLVSYLAVIVPLFNPIIYCLRNODVKRALRRLTLH 312
DB 268 PKSSHSPGMDKLALFLTYAVTSMLNPIIYSLRNKDYKALRLTL 313

RESULT 12
US-08-748-506-24
Sequence 24, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 32086
US-08-988-876-7

Query Match 36.9%; Score 623; DB 3; Length 314;
Best Local Similarity 42.4%; Pred. No. 2,8e-48;
Matches 128; Conservative 56; Mismatches 114; Indels 4; Gaps 1;

QY 10 VSEFVLGPPAPAPRLVLLFFSLDYLVLVTENMLIIAIRNHPPLHKKMYFFLANMSF 69
DB 9 ISDFLLGLPIQEQONCLVALFLAMVLTLLGNLLIIVIRDSHLHPMYFLSLMSF 68
QY 70 LEIWTYVTPKMLAGFISGENHGOISPEACMTQYFELGCTECVCLAMAYDRY 129
DB 69 SDCEFSVYIPKLQ---NMQNDPSIPADCLTQMYFFLFGDLESLVLAAYDRY 124
QY 130 AICPLHPIYVYSSRLCYVMAAGSGFGISNWKVFLISRLSYCGPNTINHFECVSP 189
DB 125 AICFPLHPIYVYSSRLCYVMAAGSGFGISNWKVFLISRLSYCGPNTINHFECVSP 184
QY 190 LNSCTDMSTAEITDVLAFILGLPLSVTGASYMAITGAVMRIPSAAGHKAFTSCSH 249
DB 185 LKLAFTDRNEMVIFIMGLIIVIPFLILGSIYARIVSILKVPSSKICKAKAFTSCSH 244
QY 250 LFWIIFVYASIFIVARPKALSAFDTNKLVSYAVIPLFNPIICLRNODYKRALRT 309
DB 245 LSVSLFTGIVGLICSSANSTLKTQVAMMYTVVTPMLNPFITSLRNODKGLSRV 304
QY 310 LHLAQ 314
DB 305 LSRVQ 306

RESULT 15
US-08-748-506-22
Sequence 22, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnelt et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voigt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 327 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-748-506-22

Query Match 36.5%; Score 616; DB 4; Length 327;
Best Local Similarity 42.0%; Pred. No. 1.3e-47;
Matches 128; Conservative 50; Mismatches 123; Indels 4; Gaps 1;

QY 10 VSEFVLGPPAPAPRLVLLFFSLDYLVLVTENMLIIAIRNHPPLHKKMYFFLANMSF 69
DB 15 VLEFIFDRFPVABHLIFELFLHLAVLSLGMNMLITTCVDHRLQTPMYFFLSMFSS 74
QY 70 LEIWTYVTPKMLAGFISGENHGOISPEACMTQYFELGCTECVCLAMAYDRY 129
DB 75 VECCFITTVIPQLITILSR---QKIPMAISQAFYLVVGATGFLVGLSLDRFL 130
QY 130 AICPLHPIYVYSSRLCYVMAAGSGFGISNWKVFLISRLSYCGPNTINHFECVSP 189
DB 131 AICFPLHPIYVYSSRLCYVMAAGSGFGISNWKVFLISRLSYCGPNTINHFECVSP 190
QY 190 LNSCTDMSTAEITDVLAFILGLPLSVTGASYMAITGAVMRIPSAAGHKAFTSCSH 249
DB 191 ANLSCSETRSIEMLEFTLAIIVFASLLIIFAYSNIVTVIPLPARERORAFSTCSSH 250
QY 250 LFWIIFVYASIFIVARPKALSAFDTNKLVSYAVIPLFNPIICLRNODYKRALRT 309
DB 251 LIVSLMTGSCATIIYKPKRORSVDINREALVNTVTPILNVIYITLRNKKVHQALRDA 310
QY 310 LHLAQ 314
DB 311 LSRVQ 315

Search completed: May 22, 2002, 15:40:20
Job time: 565 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 22, 2002, 15:33:51 ; Search time 29.43 Seconds
(without alignments)
1922.166 Million cell updates/sec

Title: us-09-771-209-76
Perfect score: 1687
Sequence: 1 MRRNRHNSGVSEFVLLGFPA.....RTLLHLAQDEANTNKGSKIG 327

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_virus:*
17: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1613	95.6	327	11	Q9QWU6
2	1498	88.8	327	4	Q9H206
3	988	58.6	314	11	Q9EPG2
4	975	57.8	316	11	Q9EPG1
5	970	57.5	316	11	Q9EPV0
6	956.5	56.7	323	13	Q57597
7	931.5	55.2	323	13	Q13036
8	741	43.9	307	11	Q9EPV1
9	739	43.7	307	11	Q9EPG7
10	738	43.6	307	11	Q9EPG9
11	735	43.4	324	11	Q9WU86
12	732.5	43.4	315	11	Q9JKA6
13	727.5	42.8	307	11	Q9EPG0
14	722	42.7	215	4	Q96R38
15	720	42.7	317	11	Q9EPG3
16	717.5	42.5			Q9EPG3 mus musculu

17	717.5	42.5	324	11	Q920G5	Q920G5 mus musculu
18	710.5	42.1	317	11	Q9EPG4	Q9EPG4 mus musculu
19	708	42.0	306	4	Q96KK4	Q96KK4 homo sapien
20	705.5	41.8	317	4	Q9H208	Q9H208 homo sapien
21	696.5	41.3	319	11	Q9QZ22	Q9QZ22 mus musculu
22	695.5	41.2	314	11	Q9EPG6	Q9EPG6 mus musculu
23	694.5	41.2	310	11	Q9EP55	Q9EP55 mus musculu
24	690	40.9	267	11	Q9ERX6	Q9ERX6 mus musculu
25	688	40.8	319	11	Q9QZ19	Q9QZ19 mus musculu
26	682	40.4	314	11	Q9EPG5	Q9EPG5 mus musculu
27	680.5	40.3	312	11	Q9E088	Q9E088 gallus gall
28	679	40.2	313	11	Q63394	Q63394 rattus norv
29	678.5	40.2	317	11	Q923R1	Q923R1 mus musculu
30	675.5	40.0	318	11	Q9QZ21	Q9QZ21 mus musculu
31	675	40.0	318	11	Q9QZ20	Q9QZ20 mus musculu
32	674	40.0	267	11	Q9ERX7	Q9ERX7 rattus norv
33	673.5	39.9	312	11	Q9QZ18	Q9QZ18 mus musculu
34	673	39.9	318	11	Q920Z2	Q920Z2 mus musculu
35	672	39.8	314	6	077756	077756 pan troglod
36	669.5	39.7	313	6	077758	077758 hylobates 1
37	667.5	39.6	308	13	Q9QX09	Q9QX09 amyctoma t
38	667.5	39.6	313	11	Q9Z1V0	Q9Z1V0 mus musculu
39	666.5	39.5	332	11	Q9E086	Q9E086 gallus gall
40	666	39.5	315	11	Q35434	Q35434 rattus norv
41	666	39.5	321	11	070266	070266 rattus norv
42	664	39.4	312	13	Q9QX10	Q9QX10 amyctoma t
43	662	39.2	129	11	Q9ESG0	Q9ESG0 mus musculu
44	661	39.2	308	11	Q9R0K3	Q9R0K3 mus musculu
45	661	39.2	321	11	070268	070268 rattus norv

ALIGNMENTS

RESULT 1
ID Q9QWU6 PRELIMINARY; PRT; 327 AA.
AC Q9QWU6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE OLFATORY RECEPTOR I7.
OS OLFR41.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BL/6;
RA Krautwurst D., Yau K.W., Reed R.R.;
RT "Identification of ligands for olfactory receptors by functional
RT expression of a receptor library."
RL Cell 95:917-926(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Lane R.P., Cutforth T., Young J., Athanasiou M., Friedman C.,
RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT "Genomic Analysis of Orthologous Mouse and Human Olfactory Receptor
RT loci Indicates Cluster Stability yet Minimal Conservation Beyond the
RT Coding Sequence."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AF106007; AAD1307.1; -;
EMBL: AF312133; AAG45187.1; -;
MGD: MGI:133840; Olfr41.
DR Interpro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECEPTOR_F1_1; UNKNOWN.1.
DR PROSITE: PS50262; G-PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor.

SEQUENCE 327 AA; 36150 MW; 4E94C75C909210E5 CRC64:

Query Match 95.6%; Score 1613; DB 11; Length 327;

Best Local Similarity 95.1%; Pred. No. 1.2e-145;

Matches 311; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

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OY 1 MERRNHSRGVSEFVLGFPAPAPRLVLFLLSLDYVLVTENMLIIAIRNHPYLHKPM 60
DB 1 MERRNHSRGVSEFVLGFPAPAPRLVLFLLSLDYVLVTENMLIIAIRNHPYLHKPM 60
OY 61 YFFLAMSFLEIWTYVTVTPKMLAGFISGENHGLISFEACMTQLYFELGCTECVLL 120
DB 61 YFFLAMSFLEIWTYVTVTPKMLAGFISGENHGLISFEACMTQLYFELGCTECVLL 120
OY 121 AVAYDRYVAICHPHYPIVSSRLCVQMAAGSMAGFGISMKVFLISRLSYCGPNTIN 180
DB 121 AVAYDRYVAICHPHYPIVSSRLCVQMAAGSMAGFGISMKVFLISRLSYCGPNTIN 180
OY 181 HFFCDVSPLLNSTCDTMSAEITDPLAIFILLGPLSVTGASYMAITGAVMRIPSAAGR 240
DB 181 HFFCDVSPLLNSTCDTMSAEITDPLAIFILLGPLSVTGASYMAITGAVMRIPSAAGR 240
OY 241 KAFSTCASHLTVTIITYAASIFIYARPKALSADTKLVSLYAVIVPLNPIITCLRNQ 300
DB 241 KAFSTCASHLTVTIITYAASIFIYARPKALSADTKLVSLYAVIVPLNPIITCLRNQ 300
OY 301 DVKRALRTLHLAQDEANTNGSKIG 327
DB 301 EVKRALRTLHLAQDGDANTKKSSRDG 327

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RESULT 2

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ID 09H206 PRELIMINARY; PRT; 327 AA.
AC 09H206:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HIT OLFACTOR RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21310002; PubMed=11416212;
RA Lane R.P., Cutforth T., Young J., Athanasios M., Friedman C.,
RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT "Genomic analysis of orthologous mouse and human olfactory receptor
RT loci."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
DR EMBL; AF321237; AAG45208.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECIP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 327 AA; 36154 MW; 9C11914D3F069FC1 CRC64:

```

Query Match 88.8%; Score 1498; DB 4; Length 327;
 Best Local Similarity 89.5%; Pred. No. 1.1e-134;
 Matches 291; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

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OY 1 MERRNHSRGVSEFVLGFPAPAPRLVLFLLSLDYVLVTENMLIIAIRNHPYLHKPM 60
DB 1 MERRNHSRGVSEFVLGFPAPAPRLVLFLLSLDYVLVTENMLIIAIRNHPYLHKPM 60
OY 61 YFFLAMSFLEIWTYVTVTPKMLAGFISGENHGLISFEACMTQLYFELGCTECVLL 120
DB 61 YFFLAMSFLEIWTYVTVTPKMLAGFISGENHGLISFEACMTQLYFELGCTECVLL 120

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OY 121 AVAYDRYVAICHPHYPIVSSRLCVQMAAGSMAGFGISMKVFLISRLSYCGPNTIN 180
DB 121 AVAYDRYVAICHPHYPIVSSRLCVQMAAGSMAGFGISMKVFLISRLSYCGPNTIN 180
OY 181 HFFCDVSPLLNSTCDTMSAEITDPLAIFILLGPLSVTGASYMAITGAVMRIPSAAGR 240
DB 181 HFFCDVSPLLNSTCDTMSAEITDPLAIFILLGPLSVTGASYMAITGAVMRIPSAAGR 240
OY 241 KAFSTCASHLTVTIITYAASIFIYARPKALSADTKLVSLYAVIVPLNPIITCLRNQ 300
DB 241 KAFSTCASHLTVTIITYAASIFIYARPKALSADTKLVSLYAVIVPLNPIITCLRNQ 300
OY 301 DVKRALRTLHLAQDEANTNGSK 325
DB 301 EVKRALCTLHLQDODPPKASR 325

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RESULT 3

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ID 09EPG2 PRELIMINARY; PRT; 314 AA.
AC 09EPG2:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE M51 OLFACTOR RECEPTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21310002; PubMed=11416212;
RA Lane R.P., Cutforth T., Young J., Athanasios M., Friedman C.,
RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT "Genomic analysis of orthologous mouse and human olfactory receptor
RT loci."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
DR EMBL; AF321234; AAG45189.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECIP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 314 AA; 35713 MW; 9E0AFB9E7F1D8CC7 CRC64:

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Query Match 58.6%; Score 988; DB 11; Length 314;
 Best Local Similarity 59.5%; Pred. No. 4.1e-86;
 Matches 179; Conservative 60; Mismatches 58; Indels 4; Gaps 1;

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OY 10 VSEFVLGFPAPAPRLVLFLLSLDYVLVTENMLIIAIRNHPYLHKPMYFPLANMSF 69
DB 9 VSEFVLGFPAPAPRLVLFLLSLDYVLVTENMLIIAIRNHPYLHKPMYFPLANMSF 68
OY 70 LEIWTYVTVTPKMLAGFISGENHGLISFEACMTQLYFELGCTECVLLAVMAYDRYV 129
DB 69 LEIWTYVTVTPKMLAGFISGENHGLISFEACMTQLYFELGCTECVLLAVMAYDRYV 124
OY 130 AICHPLHYPIVSSRLCVQMAAGSMAGFGISMKVFLISRLSYCGPNTINHPFCDVSP 189
DB 125 AICHPLHYPIVSSRLCVQMAAGSMAGFGISMKVFLISRLSYCGPNTINHPFCDVSP 184
OY 190 LNSTCDTMSAEITDPLAIFILLGPLSVTGASYMAITGAVMRIPSAAGRHAFTCASH 249
DB 185 LNSTCDTMSAEITDPLAIFILLGPLSVTGASYMAITGAVMRIPSAAGRHAFTCASH 244
OY 250 LTVIITYAASIFIYARPKALSADTKLVSLYAVIVPLNPIITCLRNQDVKRALRT 309
DB 245 LTVIITYAASIFIYARPKALSADTKLVSLYAVIVPLNPIITCLRNQDVKRALRT 304

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DR PRINTS: PR00237; GPCRHDOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECPEP_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECPEP_FL_2; 1.
 KW Receptor.
 SO SEQUENCE 307 AA; 34356 MW; 4E3FB761DCA2ACA60 CRC64;

Query Match 43.9%; Score 741; DB 11; Length 307;
 Best Local Similarity 47.8%; Pred. No. 1,4e-62;
 Matches 143; Conservative 52; Mismatches 100; Indels 4; Gaps 1;

OY 10 USEVLLGFPAPAPRLVLLFSLDYLVTENMLIIAIRNPTLHKPMYFLANNSF 69
 DB VTEFIFGLSODPQTQVLLFLEFLFYLLVGNLLIIVLHSDPRLTPMYFLRNLISF 68
 OY 70 LEIMVVTITIKMLAGIFGSKENHQLISFEACMTQLYFGLCTECCVLLAVMAYDRYV 129
 DB ADLCSTTVVQVLLVHFLVTKRT---ISFAGCTQIVVLLVCGTECALLAVMSYDRYV 124
 OY 130 AICHPHLPVIVSSRLCYOMAGSWGFGISMWKVFILSRISYCGPTINHFCDVSPL 189
 DB 125 AVCKPLHSTIMTHWVCYQLAAGSAGALVSLVDTFTLLPLRYGNVINHFCPEPAL 184
 OY 190 LNLCTDMSTAEFLDVLAFILGLPLSVTGASYMATIGAVMRIPSAAGRRKAFSTCASH 249
 DB 185 LKLSADYSTEMAIFAGVIVLLAPVSLILTSYWNIIISVYIQMGSGEGRUKVSTCGSH 244
 OY 250 LTVVLIIFAAISFIYARKKALSAFDTNKLVSLVLAIVPLFNPIIYCLRNODVKRALRR 308
 DB 245 LIVVLLFGSIFAFYMRNSKIMNEKDKMISVFSAYVPMPLNPIIYSLRNKDVGALKR 303

RESULT 9
 ID P70024 PRELIMINARY; PRT: 222 AA.
 AC P70024;
 DT 01-FEB-1997 (TREMBLREL. 02, Created)
 DT 01-FEB-1997 (TREMBLREL. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)
 DE OLFACTORY RECEPTOR (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 NC NCBL_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Freitag J.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96112032; PubMed=8845161.
 RA Freitag J., Krieger J., Scroftan J., Breer H.;
 RT "Two classes of olfactory receptors in Xenopus laevis."
 RL Neuron 15;1383-1392(1995).
 DR EMBL: Y08353; CA69639.1; -;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECPEP_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECPEP_FL_2; 1.
 KW Receptor.
 FT NON TER 1 1
 FT 222 222
 SO SEQUENCE 222 AA; 24805 MW; 7AF683570D5EBA8 CRC64;

Query Match 43.8%; Score 739; DB 13; Length 222;
 Best Local Similarity 60.4%; Pred. No. 1.5e-62;
 Matches 136; Conservative 39; Mismatches 46; Indels 4; Gaps 2;

OY 65 ANMSFLEIWTYVITPKMLAGIFGSKENHQLISFEACMTQLYFGLGTECVLLAVMA 124
 DB 1 SNMSFLEIRYISVTLPLNLLVNTL-SKD--MSISLAGCMAQLYFISIMCTECVLLAVMA 56

OY 125 YDRVAATCHPLHYPIVIVSSRLCYOMAGSWGFGISMWKVFILSRISYCGPTINHFPC 184
 DB 57 FDRYIAVCHPLHYPIVIVSSRLCYOMAGSWGFGISMWKVFILSRISYCGPTINHFPC 116
 OY 185 DVSEPLNLCTDMSTAEFLDVLAFILGLPLSVTGASYMATIGAVMRIPSAAGRRKAFS 244
 DB 117 DISVPLNLACVDMSLAEFDEVLLVILTPLEFVTVASVLCIFILKIPNTGROKAFS 176
 OY 245 TCASHLTVVITFIYARKKALSAFDTNKLVSLVLAIVPLFNPIIYCLRNODVKRALRR 289
 DB 177 TCASHLTVVITFIYARKKALSAFDTNKLVSLVLAIVPLFNPIIYCLRNODVKRALRR 221

RESULT 10
 ID Q9EP67 PRELIMINARY; PRT: 307 AA.
 AC Q9EP67;
 DT 01-MAR-2001 (TREMBLREL. 16, Created)
 DT 01-MAR-2001 (TREMBLREL. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
 DE B5 OLFACTORY RECEPTOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBL_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SVJ, AND C57BL/6J;
 RA Lane R.P., Cuthforth T., Young J., Athanasios M., Friedman C.,
 RA Rowen L., Evans G., Axel R., Hood L., Trask R.J.;
 RT "Genomic Analysis of Orthologous Mouse and Human olfactory receptor
 loci indicates Cluster stability yet Minimal Conservation Beyond the
 Coding Sequence."
 RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF321235; AAG45200.1; -;
 DR EMBL: AF321234; AAG45193.1; -;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHDOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECPEP_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECPEP_FL_2; 1.
 KW Receptor.
 SO SEQUENCE 307 AA; 34288 MW; C9C6298ED8355B85 CRC64;

Query Match 43.7%; Score 738; DB 11; Length 307;
 Best Local Similarity 47.5%; Pred. No. 2.6e-62;
 Matches 142; Conservative 52; Mismatches 101; Indels 4; Gaps 1;

OY 10 USEVLLGFPAPAPRLVLLFSLDYLVTENMLIIAIRNPTLHKPMYFLANNSF 69
 DB 9 VTEFIFGLSODPQTQVLLFLEFLFYLLVGNLLIIVLHSDPRLTPMYFLRNLISF 68
 OY 70 LEIMVVTITIKMLAGIFGSKENHQLISFEACMTQLYFGLCTECCVLLAVMAYDRYV 129
 DB ADLCSTTVVQVLLVHFLVTKRT---ISFAGCTQIVVLLVCGTECALLAVMSYDRYV 124
 OY 130 AICHPHLPVIVSSRLCYOMAGSWGFGISMWKVFILSRISYCGPTINHFCDVSPL 189
 DB 125 AVCKPLHSTIMTHWVCYQLAAGSAGALVSLVDTFTLLPLRYGNVINHFCPEPAL 184
 OY 190 LNLCTDMSTAEFLDVLAFILGLPLSVTGASYMATIGAVMRIPSAAGRRKAFSTCASH 249
 DB 185 LKLSADYSTEMAIFAGVIVLLAPVSLILTSYWNIIISVYIQMGSGEGRUKVSTCGSH 244
 OY 250 LTVVLIIFAAISFIYARKKALSAFDTNKLVSLVLAIVPLFNPIIYCLRNODVKRALRR 308
 DB 245 LIVVLLFGSIFAFYMRNSKIMNEKDKMISVFSAYVPMPLNPIIYSLRNKDVGALKR 303

RESULT 11
 Q9EP69

ID	09E9FE9	PRELIMINARY:	PRT:	307 AA.
AC	09E9FE9			
DT	01-MAR-2001	(TREMBLrel. 16, Created)		
DT	01-OCT-2001	(TREMBLrel. 18, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	B6 OLFATORY RECEPTOR.			
DE	Mus musculus (Mouse).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J			
RX	MEDLINE=21310002; PubMed=11416212;			
RA	Lane R.P., Cutforth T., Young J., Athanasios M., Friedman C.,			
RA	Rosen L., Evans G., Axel R., Hood L., Trask B.J.;			
RT	"Genomic analysis of orthologous mouse and human olfactory receptor			
RT	loci."			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).			
DR	EMBL; AF31234; AAG45194.2; -			
DR	InterPro: IPR000276; GPCR_Rhodpsn.			
DR	Pfam: PF00001; Tm1.1; 1			
DR	PRINTS; PR00237; GPCRHHODPSN.			
DR	PROSITE; PS50262; G_PROTEIN_RECPT_FL2; 1.			
RW	Receptor.			
QO	SEQUENCE	307 AA;	34243 MW;	E3A9CC87B0CDD5DC CRC64;

Query Match	Similarity	43.6%	Score 735	DB 11	Length 307
Best Local Similarity	47.5%	Pred. No. 5,1e-62			
Matches 142	Conservative 52	Mismatches 101	InDels 4	Gaps 1	
QY	10	VSEFVLGFPAPAPRLVLLFSLDDYVLVLTENMLIIAIRNHPLAKPMYEFLLANMSF	69		
Db	9	VTEFVFLGSDPQOVLLLEFFLEFLYLLTLVGNLLIIVLHSDPLRHPMFFFLCNLSF	68		
QY	70	LEIWLVTYIPLKMLAGFISCKENHQLISFEACMQLYFFLLGCECVLLVMANDRY	129		
Db	69	ADLCSTTVTPOVLLVHFLVKKRT---ISFACSTQIVLLLVGCTECALLVMSTDGYV	124		
QY	130	AICHPHLVPVIVSSRLCYOMAGSNAGGFGISVMYVFLISRLSYCGPNTINHFCDVSP	189		
Db	125	AVCKRLHSTIMTHWVCYQGLAGSNAGSLVSLVDTPTFLRLPYKGNVNIHFECRPL	184		
QY	190	LNLCTDMSTVELDPVLAIFLLGPLSVTGYAIVTGAIVRIPSAAGRHKAFTSCASH	249		
Db	185	LKLADADYVSTFEMALFFAMGVILLAPVSLITLSYMNIVSTVIOMSGEGRLKVFYSCGH	244		
QY	250	LTVVIFFAASIFETIARPKALSAPFTNKLVSLLVAVLPFLPIYCIJPNQVKKRLR	308		
Db	245	LIVLVLEFGSLFAFYMRPSKTMNKDKMISVFSNVPMLNPITYSLRNKKVKGALRR	303		
RESULT 12					
Q9WU86					
AC	Q9WU86	PRELIMINARY	PRT	324	AA.
AC	Q9WU86				
DT	01-NOV-1999	(TREMBLrel. 12, Created)			
DT	01-NOV-1999	(TREMBLrel. 12, last sequence update)			
DT	01-JUN-2001	(TREMBLrel. 17, last annotation update)			
DE	ODORANT RECEPTOR SL				
DS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	(1)				
RN	SEQUENCE FROM N.A.				
RP	STRAIN=BAIB/C				
RC	MEDLIND=99189756; PubMed=10089886;				
RX	Malnic B., Hirono J., Sato T., Buck L.B.,				
RT	"Combinatorial receptor codes for odors."				
RL	Cell 96:713-723(1999).				
EMBL	AF121972; AAD27592.1; -				

DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR000215; Serpin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE: PS00284; SERPIN; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 324 AA; 36770 MW; 30B98B4461480A34 CRC64;

Query Match 43.4%; Score 732.5; DB 11; Length 324;
Best Local Similarity 46.9%; Pred. No. 9.3e-62;
Matches 146; Conservative 47; Mismatches 113; Indels 5; Gaps 2

```

OY 1 MERRRHS--GRVSEFYLGGPAPAPARLVLLFEFFSLDYLVLTEENMIIIAIRNHPTLAKP 59
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 9 LDAMRNSAHVTEFVLGGPPGSMKIQIFLVFLVFYVLTLLGNCALICAVACDSSLHP 68
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 60 MYEFLANNSFEIWTYVVTIPKMLAGFSGSKENHGOLISFEACMQLYFPLGLCTEVL 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 69 MYELLGNSEFLTEIWTYSSTIPNMLINLSKT----KALISFGCLQPFYFFFLGTECLF 124
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 120 LAVMAYDRVVALCHPLHVAIVYSSRLCYCMAGNSAGNGGISMVWFVLSRLSYCGPNTI 179
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 125 LAVMAYDRVVALCHPLHPTIMTRRLCCILVSSCWHLGFLGPIFSLISQVPPGCSNII 184
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 180 NHFFCDVSPDLNLSCDTDSMAELTFVLAIFLLGPLVSYGASWYATGCAVRIPSAAGR 239
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 185 DHFFCDMPDLMLSCAPARITFEIFYAASSFVLFETIAIYLSYILLRAVQVPSAAGR 244
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 240 HNAEFTGASHLVVLIYFAASAEIYARPKALSAFPTNKVSYLVAVIYVFNPIIYCARN 299
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 KRAEFTCGSHLVVLSFPGTYVMVSPYIGIPIIMOKITLIVSYMPLFNPLIYSLRN 304
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 300 ODVKRALRRTL 310
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 305 KDMKLALRNL 315
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
O9UKA6
AC O9UKA6 PRELIMINARY; PRT; 315 AA.
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE OLFACTORY RECEPTOR P2.
GN OLFRL7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RC Zheng C., Feinstein P., Bozza T., Rodriguez I., Mombaerts P.;
RA "Peripheral Olfactory Projections Are Differentially Affected in Mice
RT Deficient in a Cyclic Nucleotide-gated Channel Subunit.";
RL Neuron 0:0-0(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RC Lane R.P., Cutforth T., Young J., Athanasios M., Friedman C.,
RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT "Genomic Analysis of Orthologous Mouse and Human Olfactory Receptor
RT Loci Indicates Cluster Stability yet Minimal Conservation Beyond the
RT Coding Sequence.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF247657; AAF65461.1; -.
DR EMBL; AF321233; AAG45184.1; -.
DR MGI; MGI:109148; Olfrl7.
DR InterPro; IPR000276; GPCR_Rhodopsn.

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 22, 2002, 15:19:09 ; Search time 32.83 Seconds
(Without alignments)
1106.340 Million cell updates/sec

Title: US-09-771-209-76
Perfect score: 1687
Sequence: 1 MERRHSGRSEFVLLGPPA.....RTLHLAQDEANTNGSKIG 327

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A.Geneseq.032802.*
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
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12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
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15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1671	99.1	337	13	AA27872
2	1490	88.3	337	22	AAU24727
3	1454	86.2	337	22	AA271675
4	1395	82.7	337	22	AA271683
5	1382.5	82.0	286	15	AA48744
6	1382.5	82.0	286	17	AAW02716
7	1248	74.0	278	22	AA272010
8	1248	74.0	278	22	AA272365
9	971.5	57.6	317	22	AAU24722
10	970.5	57.5	313	22	AA271777
11	957.5	56.8	301	22	AA266357

12	957.5	56.8	311	22	AA271414	Human olfactory re
13	957.5	56.8	311	22	AA272361	Human OR-like poly
14	944.5	56.0	324	22	AA271590	Human olfactory re
15	944.5	56.0	324	22	AA272179	Human OR-like poly
16	944.5	56.0	325	22	AA272463	Human olfactory re
17	923	54.7	314	22	AA271962	Human olfactory re
18	887	52.6	319	22	AA271967	Human olfactory re
19	871	51.6	330	22	AA272645	Murine OR-like pol
20	788	46.7	311	22	AA273006	Olfactory receptor
21	784	46.5	311	13	AA27869	Olfactory receptor c
22	776	46.0	317	22	AAU24626	Odorant receptor re
23	776	46.0	317	22	AA271729	Human olfactory re
24	776	46.0	317	22	AA272467	Human OR-like poly
25	774	45.9	308	22	AAU24700	Human olfactory re
26	774	45.9	308	22	AA271889	Human olfactory re
27	766.5	45.4	291	22	AA271607	Human olfactory re
28	752.5	44.6	312	22	AA271811	Novel human diagno
29	751	44.5	312	22	AA271811	Human olfactory re
30	750.5	44.5	317	22	AA273032	Olfactory receptor
31	745.5	44.2	312	22	AA271814	Human olfactory re
32	745.5	44.2	312	22	AAU24609	Human olfactory re
33	745.5	44.2	312	22	AA272585	Human G-protein co
34	743	44.0	304	22	AA271480	Human OR-like poly
35	743	44.0	304	22	AA272579	Human olfactory re
36	743	44.0	312	22	AAU24601	Human olfactory re
37	739	43.8	222	22	AA273062	Olfactory receptor
38	738	43.7	304	22	AA266385	Murine partial olf
39	736	43.6	317	22	AA271824	Human olfactory re
40	733.5	43.5	317	22	AA271931	Human olfactory re
41	733.5	43.5	322	22	AAU24728	Human olfactory re
42	730.5	43.3	314	22	AAU05133	Human odorant rece
43	730.5	43.3	314	22	AA271581	Human olfactory re
44	730	43.3	324	22	AA271913	Human G-protein co
45	730	43.3	324	22	AAU24667	Human olfactory re

ALIGNMENTS

RESULT 1		
AA27872	standard; protein; 327 AA.	
XX		
XX		
AC	AA27872:	
XX		
DT	15-MAR-1993 (first entry)	
XX		
XX		
DE	Odorant receptor clone 17.	
XX		
KW	Odorant receptor; insect; vertebrate; fish; mammal; neurotransmitter;	
KW	hormone; G-protein; surface receptor; olfactory epithelium; PCR;	
KW	Sprague-Dawley rat; amplify; primer; polymerase chain reaction;	
KW	multigene family; ligand binding domain.	
XX		
OS	Rattus rattus.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 35	/label= VAL, ALA, ASP, GLY
XX		
PN	W09217585-A.	
XX		
PD	15-OCT-1992.	
XX		
PF	06-APR-1992:	92WO-US02741.
XX		
PR	05-APR-1991:	91US-0681880.
XX		
PA	(UYCO) UNIV COLUMBIA NEW YORK.	
XX		
PI	Axel R, Buck LB;	
XX		
DR	WPI: 1992-366257/44.	

DR N-PSDB; AA029860.
XX Nucleic acid encoding an odorant receptor - can be used to
PT control insect populations or for detecting odours e.g. alcohol,
PT explosives, natural gas etc.

PS Claim 41; Fig 14; 195pp; English.

XX The sequences given in AAR27867-89 are encoded by odorant receptor
CC clones derived from an insect, a vertebrate, a fish or a mammal.
CC These clones form a family of neurotransmitters and hormone receptors
CC which transduce intracellular signals by activation of specific G-
CC proteins. Each of these receptors is a member of a superfamily of
CC surface receptors which traverse the membrane seven times. These
CC clones are only expressed in the olfactory epithelium. These clones
CC were isolated using probes derived from RNA prepared from the
CC olfactory epithelia of Sprague-Dawley rats. Isolated cDNA's were
CC amplified using primers which correspond to transmembrane domain 2
CC and 7. PCR products of the appropriate size were isolated and
CC sequenced. The deduced protein sequences of these cDNA's defined a
CC new multigene family which shared sequence and structural properties
CC with the superfamily of neurotransmitter and hormone receptors which
CC traverse the membrane seven times. This novel family, however
CC exhibits features different from any other member of the superfamily
CC identified so far. There is a striking divergence within the third,
CC fourth and fifth transmembrane domains between the olfactory proteins.
CC This divergence in the potential ligand binding domain is consistent
CC with the idea that the family of molecules cloned is capable of
CC associating with a large number of odorant of diverse molecular
CC structure.

XX Sequence 327 AA:

Query Match 99.1%; Score 1671; DB 13; Length 327;
Best Local Similarity 99.1%; Pred. No. 3.7e-187;
Matches 324; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MERRNHSGVSEFVLLGPPAPAPALVLEFSLDYLVLVTENMLITAIRNHPTLHKPM 60
DB 1 mertrhsgvsefvlilgfpapapilvllfllsllyxvlltlenmlllalnphlkhpm 60
OY 61 YFFLANMSFLEIWTYVTPKMLAGFIGSKENHGOLISFEACMTOLYFPLGCTECVLL 120
DB 61 yfflanmsflelwtvtpkmlagfigskenhgqlisfeacmtqlyffligctecvll 120
OY 121 AVMAVDRYVAICHPPLHYPIVYSSRLCVQMAAGSWAGFGISMKVYKFLISRLSYCGPNTIN 180
DB 121 avmaydryvaichpplhyvpyivssrlcvqmaagswagfgismkvkflisrlsygcpntln 180
OY 181 HFFCQVSPULNISCCTDMSTAEITDFVLAIFILGLPLSTGASYMAITGAVMRIPSAAGR 240
DB 181 hffcdvspulniscctdmstaeltfdvlaifilglplstgasymaigtavmrpsaagr 240
OY 241 KAFSTCASHLTWVITFYVASTFIYARPKALSAFDNKLVSIVYAVIVPFPNFITICLRNO 300
DB 241 kafstcashltwvityvastyfiyarpkalsafdnklvsviyavivpfpnfityclrnq 300
OY 301 DVKRALRRTLHLADQDEANTNGSKIG 327
DB 301 dvkralrrtlhladqdeantnkgiskig 327

RESULT 2
ID AAU24727 standard; Protein; 327 AA.
AC AAU24727;
XX 18-DEC-2001 (first entry)
DT Human olfactory receptor MOLFR226.
XX

KW Human; olfactory receptor; G protein-coupled receptor; GPCR; odorant;
KW food additive; cosmetic; fragrance; pharmaceutical additive.
OS Homo sapiens.
XX WO200168805-A2.
PN 20-SEP-2001.
PD 13-MAR-2001; 2001WO-US07771.

XX 13-MAR-2001; 2000US-0188914.
XX 24-MAR-2000; 2000US-0192033.
XX 12-APR-2000; 2000US-0196474.
XX 24-APR-2000; 2000US-0199335.
XX 26-MAY-2000; 2000US-0207702.
XX 23-JUN-2000; 2000US-0213849.
XX 16-AUG-2000; 2000US-0226534.
XX 07-SEP-2000; 2000US-0230732.
XX 07-FEB-2001; 2001US-0266862.

PA (SENO-) SENOMYX INC.
PI Zozulya S:
XX WPL: 2001-570867/64.
XX N-PSDB; AAS42420.

PT Nucleic acids encoding human olfactory G protein-coupled receptors,
PT useful for screening for compounds involved in olfactory sensation,
PT where the compounds can be used in the food, pharmaceutical and
PT cosmetic industries to customise odours -

XX Claim 60; Page 178; 319pp; English.

XX The invention relates to nucleic acids encoding human olfactory
XX receptors, OR (a G protein-coupled receptor, GPCR). The OR's
XX specifically recognise molecules, odorants, that elicit specific
XX olfactory sensation. The human olfactory receptors and polynucleotides
XX encoding them are useful for screening a library of chemical compounds
XX for compounds that are involved in olfactory sensation. Modulators of
XX their activity are useful for pharmacological and genetic modulation of
XX olfactory signalling pathways. Therefore, they can be used in the food,
XX pharmaceutical and cosmetic industries to customise odours and
XX fragrances. The present sequence is a human olfactory receptor of the
XX invention.

SO Sequence 327 AA:

Query Match 88.3%; Score 1490; DB 22; Length 327;
Best Local Similarity 89.2%; Pred. No. 6.2e-166;
Matches 290; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

OY 1 MERRNHSGVSEFVLLGPPAPAPALVLEFSLDYLVLVTENMLITAIRNHPTLHKPM 60
DB 1 mertrhsgvsefvlilgfpapapilvllfllsllyxvlltlenmlllalnphlkhpm 60
OY 61 YFFLANMSFLEIWTYVTPKMLAGFIGSKENHGOLISFEACMTOLYFPLGCTECVLL 120
DB 61 yfflanmsflelwtvtpkmlagfigskenhgqlisfeacmtqlyffligctecvll 120
OY 121 AVMAVDRYVAICHPPLHYPIVYSSRLCVQMAAGSWAGFGISMKVYKFLISRLSYCGPNTIN 180
DB 121 avmaydryvaichpplhyvpyivssrlcvqmaagswagfgismkvkflisrlsygcpntln 180
OY 181 HFFCQVSPULNISCCTDMSTAEITDFVLAIFILGLPLSTGASYMAITGAVMRIPSAAGR 240
DB 181 hffcdvspulniscctdmstaeltfdvlaifilglplstgasymaigtavmrpsaagr 240
OY 241 KAFSTCASHLTWVITFYVASTFIYARPKALSAFDNKLVSIVYAVIVPFPNFITICLRNO 300
DB 241 kafstcashltwvityvastyfiyarpkalsafdnklvsviyavivpfpnfityclrnq 300

[illegible][illegible]

QY 8 GRVSEFVLLGFPAPADRLVFLFELSLDYLVTLENMLIIAIRNHPRLHKKPYEFLAMN 67
 10 GEGEFVLLIGFPAPADRLVLSFARSAAYALVTENLIIAARNHSLHKPMYFVLAMN 69
 Db 68 SFLEIWTYVVTIPKMLAGTIGSKENHGLISPEACMTOLYFLGLCTECVLLAVNAYDR 127
 70 SSIETWYVLTLPKMLAGTIGSKENHGLISPEACMTOLYFLGLCTECVLLAVNAYDR 129
 QY 128 YVAICHPHYVIVSSRLCVOMAGSMAGFGISMWKVFELISRLSYCGPNTINHFCVDVS 187
 130 YMAICGPIHYPIVIVSGRLCVMAAGSWAGFGISMWKVFELISRLSYCGPNTINHFCVDVS 189
 Db 188 PLINISCTDMSTAEITDPEVLAIFILLGPIUSVTGASYMAITGAVMRIPSAAGRHAFTSCA 247
 190 PLINISCTDMSTAEITDPEVLAIFILLGPIUSVTGASYMAITGAVMRIPSAAGRHAFTSCA 249
 QY 248 SHLTWYIIFYAASIFYARPKALSAFDNKLIVSLAVIVPLFNPIIYCLRNODVRAIR 307
 250 SHLTWYIIFYAASIFYARPKALSAFDNKLIVSLAVIVPLFNPIIYCLRNODVRAIR 309
 QY 308 RFLHLAQDOEANTNKGSK 325
 310 CTLHYGHDQDPKKASR 327
 Db
 RESULT 5
 AAR48744
 ID AAR48744 standard; Protein; 286 AA.
 AC AAR48744;
 XX
 DF 07-JUN-1996 (first entry)
 XX
 DE G-protein coupled odorant receptor 17 protein.
 XX
 KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW psychotonic disorder; schizophrenia; dopamine; AMP; adenosine; thionin;
 KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
 KW rhodopsin; opsin; odorant; cytomagalovirus.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 9 */note= "unknown amino acid"
 XX
 PN WO9405695-A1.
 XX
 PD 17-MAR-1994.
 XX
 PF 09-SEP-1993; 93WO-US08528.
 XX
 PR 10-SEP-1992; 92US-0943236.
 XX
 PA (UYNY) UNITV NEW YORK STATE.
 XX
 PI Murphy RB, Schuster DI;
 XX
 DR WPI: 1994-101120/12.
 XX
 PT Polypeptides of G-coupled receptor proteins (GPRs) - useful for
 binding GPR ligands or modulating GPR binding
 XX
 PS Disclosure: Page 120; 160pp; English.
 CC Proteins AAR48685-R48758 represent a range of G-protein coupled receptor
 CC proteins selected from CAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thionin, endothelin, bombesin, endocrine, rhodopsin, opsin,
 CC odorant, cytomagalovirus and other G-protein coupled receptors. The
 CC receptor proteins were used to design polypeptides, pref. based on the
 CC transmembrane domains, for use in G-protein coupled receptor ligand
 CC binding assays. The polypeptide fragments retain biological activity

CC such as binding a GPR ligand or modulating GPR ligand binding to a GPR
 CC (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples
 CC of polypeptide fragments). The polypeptide fragments can be used in
 CC compositions for treating subjects suffering from a pathology related to
 CC a GPR abnormality e.g. a psychotonic disorder such as schizophrenia.
 XX
 SQ Sequence 286 AA:
 Query Match 82.0%; Score 1382.5; DB 15; Length 286;
 Best Local Similarity 91.7%; Pred. No. 2,1e-153;
 Matches 276; Conservative 4; Mismatches 6; Indels 15; Gaps 4;
 QY 27 LFEFLSDYLVLTENMLIIAIRNHPRLHKKPYEFLAMNSFLEIWTYVVTIPKMLAGF 86
 1 LFFLSLKYVLYLTENMLIIAIRNHPRLHKKPYEFLAMNSFLEIWTYVVTIPKMLAGF 86
 Db 87 IGSKENHGLISPEACMTOLYFLGLCTECVLLAVNAYDRVATCRPHIYVIVSSRLC 146
 56 IGSKENHGLISPEACMTOLYFLGLCTECVLLAVNAYDRVATCRPHIYVIVSSRLC 115
 Db 147 YOMAGSMAGFGISMWKVFELISRLSYCGPNTINHFCVDVPLNLSCTDMSTAEITDPEV 206
 116 V---LGSWAGFGISMWKVFELISRLSYCGPNTINHFCVDVPLNLSCTDMSTAEITDPEV 172
 QY 207 LAIFILLGPIUSVTGASYMAITGAVMRIPSAAGRHAFTSCASHLVIIIFYAASIFYAR 266
 173 LAIFILLGPIUSVTGASYMAITGAVMRIPSAAGRHAFTSCASHLVIIIFYAASIFYAR 225
 Db 267 PKALSAFDNKLIVSLAVIVPLFNPIIYCLRNODVRAIRLHQAQOENANTNKGSKI 326
 226 PKALSAFDNKLIVSLAVIVPLFNPIIYCLRNODVRAIRLHQAQOENANTNKGSKI 285
 QY 327 G 327
 286 g 286
 Db
 RESULT 6
 AAM02716
 ID AAM02716 standard; peptide; 286 AA.
 AC AAM02716;
 XX
 DT 13-NOV-1996 (first entry)
 XX
 DE G-protein coupled odorant receptor 17.
 XX
 KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW schizophrenia; dopamine; AMP; adenosine; thionin; adrenergic; opsin;
 KW muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
 KW odorant; cytomagalovirus; serotoninergic.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 9 */note= "unknown amino acid"
 XX
 PN US5508384-A.
 XX
 PD 16-APR-1996.
 XX
 PF 10-SEP-1992; 92US-0943236.
 XX
 PR 09-SEP-1993; 93US-0118270.
 XX
 PA (UYNY) UNITV NEW YORK STATE..
 XX
 PI Murphy RB, Schuster DI;
 XX
 DR WPI: 1996-208785/21.

XX New dopamine receptor peptide - useful as antipsychotic agent, e.g.
 PT for treating schizophrenia
 XX
 PS Disclosure; Column 153-156; 184pp; English.
 CC Proteins AAM02657-W02730 represent a range of G-protein coupled receptor
 CC (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
 CC odorant, cytomagaloviral and other GPR proteins. The receptor proteins
 CC were used to design polypeptides, pref. based on the transmembrane
 CC domains, for use in G-protein coupled receptor ligand binding assays.
 CC The polypeptide fragments retain biological activity such as binding a
 CC GPR ligand or modulating GPR ligand binding to a GPR (see
 CC AAM02747-W02999 for examples of polypeptide fragments). The polypeptide
 CC fragments can be used in compositions for treating subjects suffering
 CC from a pathology related to a GPR abnormality e.g. a psychotic disorder
 CC such as schizophrenia.
 CC
 XX
 SQ Sequence 286 AA;
 Query Match 82.0%; Score 1382.5; DB 17; Length 286;
 Best Local Similarity 91.7%; Pred. No. 2,1e-153;
 Matches 276; Conservative 4; Mismatches 6; Indels 15; Gaps 4;
 QY 27 LLEFLSLDYLVLVTEENMLIIAIRNPTLHKPMYFELANMSFLEIYVTVITPKMLAGF 86
 Db 1 |||f||s||l||x||y||v||t||e||n||m||l||i||a||i||r||n||p||t||l||h||k||p||m||y||f||e||l||a||n||m||s||f||e||i||y||v||t||v||i||t||p||k||m||l||a||g||f||
 QY 87 IGSKENHGQILISFEACMTQLYFFELGCTECVLAVMAYDRYVAICHPLHYPIVSSRLC 146
 Db 56 |gskenhgqilistfacmtqlyfflglgctecvlla vmaydryvaichplhyvissrlz 115
 QY 147 VQMAAGSWAGGFGISMKVFLISRLSYCGPRTINHFCDVSPILNSTCDTMSIAELTDFV 206
 Db 116 v---lgs waagfgis mwkvlisrlsy cgp rti nhfcdv spl nstcdm staeltdfv 172
 QY 207 LAIFILGPISVTGAASVMTGAAMRIPSAAGRHKAFTSCASHLTVAITFYAASIFFYAR 266
 Db 173 |a|f|i|l|g|p|i|s|v|t|g|a|a|s|v|m|t|g|a|a|m|r|i|p|s|a|a|g|r|h|k|a|f|t|s|c|a|s|h|t|v|a|i|t|f|y|a|a|i|f|y|a|r|
 QY 267 PKALSAFDTNKIVSLVLAIVTPLEFNPIIYCLRNODVKRALRRLHLAODQEAANTNKGSKI 326
 Db 226 |p|k|a|l|s|a|f|d|t|n|k|i|v|s|l|v|l|a|i|v|t|p|l|e|f|n|p|i|i|y|c|l|r|n|o|d|v|k|r|a|l|r|r|l|h|l|a|o|d|e|a|n|t|n|k|g|s|k|i|
 QY 327 G 327
 Db 286 g 286
 RESULT 7
 AAG72010
 ID AAG72010 standard; Protein; 278 AA.
 XX
 AC AAG72010;
 XX
 DT 30-JUL-2001 (first entry)
 DE Human olfactory receptor polypeptide, SEQ ID NO: 1691.
 XX
 KW Human: olfactory receptor; OR: primary scent determination;
 KM secondary scent determination; polypeptide library; odour receptor;
 XX scent profile; scent fingerprint; scent representation.
 OS Homo sapiens.
 XX
 PN WO200127158-A2.
 XX
 PD 19-Apr-2001.
 XX
 PF 06-OCT-2000; 2000WO-US27582.
 XX

PR 08-OCT-1999; 99US-0158615.
 PR 24-FEB-2000; 2000US-0184809.
 XX
 PA (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 DR WPI; 2001-290713/30.
 PT New polynucleotides which encode polypeptides involved in olfactory
 PS sensation for identifying olfactory agonists and antagonists -
 CC Claim 11; Page 1102-1103; 1857pp; English.
 CC
 CC The present sequence is an olfactory receptor which is encoded by
 CC one of a number of novel polynucleotides. The polynucleotides can be
 CC used in screening for olfactory agonists and antagonists. The methods
 CC allow for the determination of primary scents and the identification
 CC of the odour receptors used to detect these primary scents. The methods
 CC also enable determination of secondary scents and the identification of
 CC combinations of odour receptors that are involved in detecting such
 CC secondary scents. This enables the construction of a scent representation
 CC (also called a scent fingerprint or scent profile), which may be used to
 CC re-create and edit scents. Libraries of olfactory receptors are useful
 CC for determining the interaction pattern of a composition with the
 CC receptors, and can be used for determining differences in the olfactory
 CC faculties of different individuals.
 CC
 XX
 SQ Sequence 278 AA;
 Query Match 74.0%; Score 1248; DB 22; Length 278;
 Best Local Similarity 87.4%; Pred. No. 1.2e-137;
 Matches 243; Conservative 13; Mismatches 22; Indels 0; Gaps 0;
 QY 48 IAIRNHPTLHKPMYFELANMSFLEIYVTVITPKMLAGFISKENHGQILISFEACMTQLY 107
 Db 1 |a|i|r|n|h|p|t|l|h|k|p|m|y|f|e|l|a|n|m|s|f|e|i|y|v|t|v|i|t|p|k|m|l|a|g|f|i|s|k|e|n|h|g|q|i|l|i|s|f|e|a|c|m|t|q|l|y|
 QY 108 FFIUGLCTECVLAVMAYDRYVAICHPLHYPIVSSRLCQVMAAGSWAGGFGISMKVFL 167
 Db 61 |f|i|g|l|g|c|t|e|c|v|l|a|v|m|a|y|d|r|y|v|i|c|h|p|l|h|y|p|i|v|s|s|r|l|c|q|v|m|a|a|g|s|w|a|g|g|f|i|s|m|k|v|f|l|
 QY 168 ISRLSYCGPRTINHFCDVSPILNSTCDTMSIAELTDFVLAIFILGPISVTGAASVMT 227
 Db 121 |s|g|l|s|y|c|g|p|r|t|i|n|h|f|c|d|v|s|p|i|l|n|s|t|c|d|m|s|i|a|e|l|t|d|f|v|l|a|i|f|i|l|g|p|i|s|v|t|g|a|a|s|v|m|t|
 QY 228 GAVMARIPSAAGRHKAFTSCASHLTVAITFYAASIFFYARPKALSAFDTNKIVSLVLAIV 287
 Db 181 |g|a|v|m|a|r|i|p|s|a|a|g|r|h|k|a|f|t|s|c|a|s|h|t|v|i|t|f|y|a|a|i|f|y|a|r|p|k|a|l|s|a|f|d|t|n|k|i|v|s|l|v|l|a|i|v|
 QY 288 PFNPIIYCLRNODVKRALRRLHLAODQEAANTNKGSKI 325
 Db 241 |p|f|n|p|i|i|y|c|l|r|n|o|d|v|k|r|a|l|r|r|l|h|l|a|o|d|e|a|n|t|n|k|g|s|k|i|
 RESULT 8
 AAG72365
 ID AAG72365 standard; Protein; 278 AA.
 XX
 AC AAG72365;
 XX
 DT 30-JUL-2001 (first entry)
 DE Human OR-like polypeptide query sequence, SEQ ID NO: 2046.
 XX
 KW Human: olfactory receptor; OR: primary scent determination;
 KM secondary scent determination; polypeptide library; odour receptor;
 XX scent profile; scent fingerprint; scent representation.
 OS Homo sapiens.
 XX

PM WO200127158-A2.
XX
PD 19-APR-2001.
XX
XX 06-OCT-2000; 2000WO-US27582.
PF
XX 08-OCT-1999; 99US-0158615.
PR 24-FEB-2000; 2000US-0184809.
XX
XX (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
XX WPI: 2001-290713/30.
DR
XX
XX New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
PT
XX
XX Example 6; Page 1371-1372; 1857pp; English.
XX
XX The present sequence is a polypeptide encoded by one of 344 newly mined
CC human genes. It was used as a query sequence in a database search of
CC olfactory receptor (OR)-like sequences. The invention relates to isolated
CC polynucleotides encoding polypeptides involved in olfactory sensation.
CC The polynucleotides can be used in screening for olfactory agonists and
CC antagonists. The methods allow for the determination of primary scents
CC and the identification of the odour receptors used to detect these
CC primary scents. The methods also enable determination of secondary scents
CC and the identification of combinations of odour receptors that are
CC involved in detecting such secondary scents. This enables the
CC construction of a scent representation (also called a scent fingerprint
CC or scent profile), which may be used to re-create and edit scents.
CC Libraries of olfactory receptors are useful for determining the
CC interaction pattern of a composition with the receptors, and can be
CC used for determining differences in the olfactory faculties of different
CC individuals.
XX
XX Sequence 278 AA:
SQ
Query Match 74.0%; Score 1248; DB 22; Length 278;
Best Local Similarity 87.4%; Pred. No. 1,2e-137;
Matches 243; Conservative 13; Mismatches 22; Indels 0; Gaps 0;
QY 48 IAINRHPPLHMKPMYFFELANMSELEIYVTVTPKMLAGFSGKENHGOLISFEACMTOLY 107
DB 1 mairnhtlkhpmgyfflaamstfelaivylvtpkmlagfsgkqhgqlisfegcmqlq 60
QY 108 PFLGAGCTBEVLLAVMAVDRYVAICHPLHYPIYVSSRLCVQMAAGSMAGSGISMWKVL 167
DB 61 fflgagctecvllavmandrymaicylhnpvlysgrlcvqmaagswagfigismkvfl 120
QY 168 ISRLSYCGPNTNHFECDDVSPILNLSCTDMSTAEILDVLAIFILLGPIVSGASYMAT 227
DB 121 lsglsgnpgnlnhlfcdvspilnlsctdmstaeildvllaifillgpiivsgasyvalt 180
QY 228 GAVMRIPSAAGRHKAFCSCASHLVVILFYAASIFVAPRKALSAFDTNKLVSVLAVIV 287
DB 181 gavlmlpsaagrykafscashlvvllfyaaasifvayprkalsafdtnkvlsvlyaviv 240
QY 268 PLEFNPIIICLRQDVKRALRRTLHLAQQDOEANTNKGSK 325
DB 241 plfnpiilyclnrqevkralccilhlhynqdpdkkgsr 278

XX
DE Human olfactory receptor AOLF221.
XX
XX Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
KW food additive; cosmetic; fragrance; pharmaceutical additive.
XX
XX Homo sapiens.
XX
XX WO200168805-A2.
XX
XX 20-SEP-2001.
XX
XX 13-MAR-2001; 2001WO-US07771.
XX
XX 13-MAR-2000; 2000US-0188914.
XX 24-MAR-2000; 2000US-0192033.
PR 12-APR-2000; 2000US-0198474.
PR 26-APR-2000; 2000US-0199335.
PR 26-MAY-2000; 2000US-0207702.
PR 23-JUN-2000; 2000US-0213849.
PR 16-AUG-2000; 2000US-0226534.
PR 07-SEP-2000; 2000US-0230732.
PR 07-FEB-2001; 2001US-0266862.
XX
XX (SENO-) SENOMTX INC.
PA
XX Zozulya S;
PI
XX WPI: 2001-570867/64.
XX N-PSDB; AAS42415.
DR
XX
XX Nucleic acids encoding human olfactory G protein-coupled receptors,
PT useful for screening for compounds involved in olfactory sensation,
PT where the compounds can be used in the food, pharmaceutical and
PT cosmetic industries to customise odours -
XX
XX Claim 60; Page 176; 319pp; English.
XX
XX The invention relates to nucleic acids encoding human olfactory
CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
CC specifically recognise molecules, odourants, that elicit specific
CC olfactory sensation. The human olfactory receptors and polynucleotides
CC encoding them are useful for screening a library of chemical compounds
CC for compounds that are involved in olfactory sensation. Modulators of
CC their activity are useful for pharmacological and genetic modulation of
CC olfactory signalling pathways. Therefore, they can be used in the food,
CC pharmaceutical and cosmetic industries to customise odours and
CC fragrances. The present sequence is a human olfactory receptor of the
CC invention.
XX
XX Sequence 317 AA:
SQ
Query Match 57.6%; Score 971.5; DB 22; Length 317;
Best Local Similarity 57.1%; Pred. No. 3.8e-105;
Matches 181; Conservative 55; Mismatches 72; Indels 9; Gaps 3;
QY 4 RNHS-GRVSEFVLGFPAPARVLFLFLSLDYLVLNENMLIIAIRNHPPLHMKPMYF 62
DB 2 lnsqsgnheeflvfgfptcpqlqlllffvlfaiyltllenllyftlwlapslnrmpyf 61
QY 63 FLANMSFLEIYVTVTPKMLAGFSGKENHGOLISFEACMTOLYFPLGAGCTBEVLLAV 122
DB 62 flhlsflelwyinvtlpillafl-----tgdgrsvyvgcmqllyffllaactecvllaiv 117
QY 123 MAYDRYVAICHPLHYPIYVSSRLCVQMAAGSMAGSGISMWKVLISRLSYCGPNTNHF 182
DB 118 maydryvaicplhlypivssrlcvqmaagswagfigismkvflisrlsygcpnlnhlf 177
QY 183 FCDVSPILNLSCTDMSTAEILDVLAIFILLGPIVSGASYMATGAVMRIPSAAGRHKA 242
DB 178 fcdvspilnlsctdmstaeltdvllaifillgpiivsgasymatgavmrripsaagrha 237

Db	62	fghstsflelwylnvtlpllaafl-----tqdgysyvgcmqjlyffllaacteccllav	117
Qy	123	MAYDRYVALCHPLHYPVIVSSRLCYOMAAAGSNAGGFGISMVKVELISLSTCGPNTINH	182
Db	118	maydrvalatcpglllypslmpsslatrclaasvsgfssmmkllffsqlyscgpnlnht	177
Qy	183	PCDVSPLNLSTDMSTAEIPLTFVLAIFILLEGPLSTGASVYAAITGAVNRIPSAARHKA	242
Db	178	fcdispllnlntcsdkegealvdflalavmlilpllavssyalaalilrplrsyrhka	237
Qy	243	FSTCSHLTVVLIIFAAASIFIVARPKALSAFPTNKLVSVLVAVIVPELPNPIYCLERNODY	302
Db	238	fstcshlavlavvlyssclfyarpramyltnhknkialvlyclivpfmpalylclnkev	297
Qy	303	KRALRRTL 310	
Db	298	keafkrktv 305	
RESULT	11		
ID	AAG66357		
XX	AAG66357	standard; Protein; 301 AA.	
AC	AAG66357;		
DT	15-OCT-2001	(first entry)	
XX			
DE	Human olfactory receptor C6 partial protein.		
XX			
KM	NOV; olfactory; cytostatic; immunomodulator; vulnery; anti-HIV;		
KM	antiaesthetic; antilinfiammatory; gastrointestinal; neuroprotective;		
KM	osteopethic; gene therapy; odorant receptor; olfactory receptor;		
KM	G-protein coupled receptor; GPCR; neuro-olfactory; trauma; human;		
KM	neoplastic disorder; cancer; adenocarcinoma; lymphoma; prostate cancer;		
KM	uterus cancer; immune response; AIDS; asthma; Crohn's disease;		
XX	multiple sclerosis; Albright hereditary osteodystrophy.		
OS	Homo sapiens.		
PN	MO200155179-A2.		
XX			
PD	02-AUG-2001.		
XX			
PF	29-JAN-2001; 2001WO-US02849.		
PR	27-JAN-2000; 2000US-0178370.		
PR	27-JAN-2000; 2000US-0178371.		
PR	27-JAN-2000; 2000US-0178406.		
PR	27-JAN-2000; 2000US-0178408.		
PR	27-JAN-2000; 2000US-0178409.		
PR	27-JAN-2000; 2000US-0178413.		
PR	27-JAN-2000; 2000US-0178414.		
PR	07-FEB-2000; 2000US-0180634.		
PR	24-JUL-2000; 2000US-0220516.		
PR	28-JUL-2000; 2000US-0221408.		
PR	31-JUL-2000; 2000US-0221943.		
PR	21-DEC-2000; 2000US-0257599.		
PR	08-JAN-2001; 2001US-0260290.		
XX			
PA	(CURA-) CURAGEN CORP.		
XX			

XX WPI: 2001-514556/56.
DR
XX
XX New NOXV polypeptides and polynucleotides, useful for treating or
PT preventing a syndrome associated with a human disease (e.g. disorders
PT of the neuro-olfactory system), as well as in gene therapy -
XX
XX
PS Disclosure: Page 58: 242pp: English.
XX
XX
CC The present invention relates to novel human NOXV proteins and coding

PN WO200127158-A2.
XX
XX 19-APR-2001.
PD
XX 06-OCT-2000; 2000WO-US27582.
PF
XX 08-OCT-1999; 99US-0158615.
PR 24-FEB-2000; 2000US-0184809.
XX
XX (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
PI WPI; 2001-290713/30.
XX
XX New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
XX
XX Example 6; Page 1368-1369; 1857pp; English.
XX
XX The present sequence is a polypeptide encoded by one of 344 newly mined
CC human genes. It was used as a query sequence in a database search of
CC olfactory receptor (OR)-like sequences. The invention relates to isolated
CC polynucleotides encoding polypeptides involved in olfactory sensation.
CC The polynucleotides can be used in screening for olfactory agonists and
CC antagonists. The methods allow for the determination of primary scents
CC and the identification of the odour receptors used to detect these
CC primary scents. The methods also enable determination of secondary scents
CC and the identification of combinations of odour receptors that are
CC involved in detecting such secondary scents. This enables the
CC construction of a scent representation (also called a scent fingerprint
CC or scent profile), which may be used to re-create and edit scents.
CC Libraries of olfactory receptors are useful for determining the
CC interaction pattern of a composition with the receptors, and can be
CC used for determining differences in the olfactory faculties of different
CC individuals.
XX
XX Sequence 311 AA:
SQ

Query Match 56.8%; Score 957.5; DB 22; Length 311;
Best Local Similarity 56.8%; Pred. No. 1.6e-103;
Matches 175; Conservative 54; Mismatches 72; Indels 7; Gaps 3;

QY 1 MERNHSGRSEFVLGFPAPARVLFLSLDYLVLLENLIIAIRNHTLAKPM 60
Db 1 melengt-rytkllivgfpsslmraamflilvayillvaenvillilvqnrlphkpm 59
XX
QY YFPLANSPLEIWTYVTPKMLAGTSGKENHGQLISFEACMTQLYFFLGCTECVL 120
Db 60 yffianisfletwyistvtpkllifswsvms----isfclmqlyffiallmctevll 115
XX
QY 121 AWMAVDRYVAICHPDLHVPVIVSSRLCYOMAGSAGFGISMWKVFILSRISYCGPMTIN 180
Db 116 aamaydyvaicrplhlyptlmsbqlcfrlalswaigfislakifysclsfscgpnvin 175
XX
QY 181 HFFCDVSPPLNLSTCDMSTAEIPLDFVLAIFLLGPLSVTGASVYMAITGAWMRIPSAGR 240
Db 176 hffcdispvnlstcdmstaelvoflialvlfifplifvlsygcclatlcmpt--gkq 233
XX
QY 241 KAFSTCASHLTUVIIFFAASIFIYARPKALSAFDTNKLVSVLAVIPLNPITTYCLRNQ 300
Db 234 kafstcshltuvvifvsaifimayprvlnahfmnkllsfyavivpsnplfyclntr 293
XX
QY 301 DVKRALRR 308
Db 294 evkealkk 301
XX
RESULT 14
AAG71590
ID AAG71590 standard; Protein: 324 AA.

XX
XX AAG71590;
AC
XX 30-JUL-2001 (first entry)
DT
XX
XX Human olfactory receptor polypeptide, SEQ ID NO: 1271.
DE
XX
XX Human: olfactory receptor; OR: primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KM scent profile; scent fingerprint; scent representation.
XX
XX Homo sapiens.
OS
XX
XX WO200127158-A2.
PN
XX 19-APR-2001.
PD
XX
XX 06-OCT-2000; 2000WO-US27582.
PF
XX
XX 08-OCT-1999; 99US-0158615.
PR 24-FEB-2000; 2000US-0184809.
XX
XX (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX WPI; 2001-290713/30.
DR
XX
XX New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
XX
XX Claim 11; Page 770-771; 1857pp; English.
PS
XX
XX The present sequence is an olfactory receptor which is encoded by
CC one of a number of novel polynucleotides. The polynucleotides can be
CC used in screening for olfactory agonists and antagonists. The methods
CC allow for the determination of primary scents and the identification
CC of the odour receptors used to detect these primary scents. The methods
CC also enable determination of secondary scents and the identification of
CC combinations of odour receptors that are involved in detecting such
CC secondary scents. This enables the construction of a scent representation
CC (also called a scent fingerprint or scent profile), which may be used to
CC re-create and edit scents. Libraries of olfactory receptors are useful
CC for determining the interaction pattern of a composition with the
CC receptors, and can be used for determining differences in the olfactory
CC faculties of different individuals.
XX
XX Sequence 324 AA:
SQ

Query Match 56.0%; Score 944.5; DB 22; Length 324;
Best Local Similarity 57.2%; Pred. No. 5.0e-102;
Matches 178; Conservative 54; Mismatches 74; Indels 5; Gaps 2;

QY 1 MERNHSGRSEFVLGFPAPARVLFLSLDYLVLLENLIIAIRNHTLAKPM 60
Db 6 levdnht-vtrfllilgfpctpaqgllffsfiflatytlitlenllilalhsdgqlkpm 64
XX
QY YFPLANSPLEIWTYVTPKMLAGTSGKENHGQLISFEACMTQLYFFLGCTECVL 120
Db 65 yffishisflemwyvtrvlskplmvdfl----shdksisfngcmqlyffvtfvcteyll 120
XX
QY 121 AWMAVDRYVAICHPDLHVPVIVSSRLCYOMAGSAGFGISMWKVFILSRISYCGPMTIN 180
Db 121 aimaifdyvaicrplhlyptlmsbqlcfrlalswaigfislakifysclsfscgpnvin 180
XX
QY 181 HFFCDVSPPLNLSTCDMSTAEIPLDFVLAIFLLGPLSVTGASVYMAITGAWMRIPSAGR 240
Db 181 hffcdispvnlstcdmstaelvoflialvlfifplifvlsygcclatlcmpt--gkq 240
XX
QY 241 KAFSTCASHLTUVIIFFAASIFIYARPKALSAFDTNKLVSVLAVIPLNPITTYCLRNQ 300
Db 241 kafstcshltuvvifvsaifimayprvlnahfmnkllsfyavivpsnplfyclntr 293
XX

Db 241 kafstcaashlevallfysmllfyarpklmaynsnkvasvlyevipllmliylclrmh 300

Qy 301 DYKRALRRLH 311 .

Db 301 evkaalrkth 311

RESULT 15
AAG72479

ID	AAG72479	standard; Protein; 324 AA.
XY		

AC AAG72479;

DT 30-JUL-2001 (first entry)
xx

Human OR-1-like polypeptide query sequence, SEQ ID NO: 2160.

KW Human; olfactory receptor; OR; primary scent determination;
 KW secondary scent determination; polypeptide library; odour receptor
 KW scent profile; scent fingerprint; scent representation.

OS Homo sapiens.

PN W0200127158-A2.

PD 19-APR-2001.

PF 06-OCT-2000; 2000WO-US27582.

PR 08-OCT-1999; 99US-0158615.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

DR WPI; 2001-290713/30.

PT New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists -

Example 6; Page 1452-1453; 1857pp; English.

The present sequence is a polypeptide encoded by one of 344 newly mined human genes. It was used as a query sequence in a database search of olfactory receptor (OR)-like sequences. The invention relates to isolated polynucleotides encoding polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different individuals.

SQ Sequence 324 AA;

Query Match	56.0%;	Score 944.5;	DB 22;	Length 324;
-------------	--------	--------------	--------	-------------

Matches 178; Conservative 54; Mismatches 74; Indels 5; Gaps 2;

QY 1 MERRNHSGRVSEFVLLGEPAPAPLRVLLFELSLDYVLVTENMLIIAIRNHPTLHKPM 600

Db 6 levdnht-vttrflllgfptrpafqllffsiflaty1ltllen11ilainhsdgqlhkpmp 64

QY 61 YFFLANMSFLEIWVVTIPKMLAGFIGSKENHGOLISFEACMTOLYFFELGLGCTECVLL 120

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Db      65  yfflshlsiflemwyvvtvlsapkmldvfl-----shdkssifngcmtdqlyffftvfcoteyll 120
OY      121  AVMANDRVVAICHPHLHRYVITYSSRLCYQMAAGSMWAGGFGISMVKVFLISLSTSCGPTIN 180
Db      121  aimadfrvaicmptirypvmtncqldgltlgaqcfvgjlmfamlmwfiaqdhycmnpn 180
OY      181  HFPCDVSFLNLSCSTDMSIAELDFVLAIFLLGLPLSLVTGASWMAITGAVMRIPSAGRH 240
Db      181  hyfcdislplnvscedsgseamwdfllamvialplcvvaasyaallatllrlrpsaqrg 240
OY      241  KAFSCASHLEVVILTFEFAASIFETARYARKALSAEDTNKVLAVLAIVPLFNPPIITCYLRNO 300
Db      241  kafscasahlvllvllfysmtilfyarplmgyansokvvasvlytlvaplmlpnylylcnrh 300
OY      301  DVKRALRRQLH 311
Db      301  evkaalrkcln 311

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Search completed: May 22, 2002, 15:40:00
Job time: 1251 sec
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